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Best Local Similarity 51.4%: Pred. No. 0.00e+00;
Matches 246; Conservative 112; Mismatches 100; Indels 21; Gaps 14

Db      69 YGSTLTSLAFTSESG-SSSLAGFHS-LNNVPSPVVFLOTAPOLPFIHHSSQVPEYL 126
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      43 YPAMTF-YSPAVMNMYSINVTNLEGGCGROTTSPNVLMPGHLSPLYVHR-QLSHLYA 100
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      127 ENEOGSFCMREAPAPFAPRPSDDNRHHSIRRMGSTNKGSLSMESTRETRYCAVCNDYA 186
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      101 EPQKSPCEANSLSEHTL-PVNRETLKRVSGNRCASPTGP-G--SKDAHFCVCSDYA 156
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      187 SGYHYGVMSCEGCKAFKFRSIQGHNDYWCAPTNOCTIDKNRKSQCAQLKCYEVMGMK 246
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      157 SGYHYGVMSCEGCKAFKFRSIQGHNDYICPATNCTIDKNRKSQCAQLKCYEVMGMK 216
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      247 GGIKRDRCGGEMMKRQREODSDNGASSTELRAPLMTSPLYVHKHKNKNSPALSITA 306
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      217 CGSRRERCGYRIYVRQRADQLHCAGKAKRSGGAPVR-E-LLL---D--ALS-P 265
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      307 EQMVALLEAEPIIYSEYDNPENPEKSMMTLTNLNADRELHYHIMAKKRVGFVDLT 366
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      266 EQLVLTLLAEAPHPLIS-RSAPPTESAMMSLTKLADKRLVHMISAKKIPFVELSL 324
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      367 HDQVHLECAMLEIMTICLVMSMEHPGKLLPAPMLLDNRQKCVSGWEIFDMLLATA 426
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      325 FDQVLTLESCEWVEYLMGLMWRSIDHPKLLFAPDLVYDRREGKVEGILIEIPMLLAT 384
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      427 AFRFMANLQGEFEVLFKSIILNSGVYFELSTLSEERDYIHRVLDKIDTLHLMK 486
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      385 SRFRLKIQHKRYELCYKAMILLNSMTYLVLTATQADDSKRLAH-LLNAVYDALWYIAK 443
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      487 SGLSLQGGHRRLAQLLLILSHIRHMSNGMEHLVNMCKNVPLYLDDLEMLADHRLA 545
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      444 SGISQOOSMRLANLMLLSHVHRASNGMEHLNMCKNVVYVYDILLEMLNAHLRG 502
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      2      STANDARD:      PRT:      595 AA.
AC      P03372.
DT      21-JUL-1986 (REL. 01, CREATED)
DT      01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR).
EN      ESR1 OR ESR.
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUHERIA; PRIMATES.
      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 86129927.
RX      GREENE G.L., GILMA P., WATERFIELD M., BAKER A., HORT Y., SHINE J.;
RA      SCIENCE 231:1150-1154(1986).
      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 86146892.
RX      GREEN S., WALTER P., KOMAR V., KRUST A., BORNERT J.-M., ARGOS P.,
RA      CHAMBER P.;
RL      NATURE 320:134-139(1986).
      [3]
RP      STRUCTURE BY NMR OF 180-262.
RX      MEDLINE: 91061891.
RA      SCHWABE J.W.F., NEUHAUS D., RHODES D.;
RL      NATURE 348:458-461(1990).
      [4]
RP      VARIANT VAL-400.
RX      MEDLINE: 900054402.
RA      TOBA L., MULLICK A., METZGER D., PONGLIKITMONGKOL M., PARK I.,
RA      CHAMBER P.;
RL      EMBO J. 8:1981-1986(1989).
      [5]
RP      VARIANT ALA-447.
RX      MEDLINE: 92250650.
RA      REESE J.C., KATZENELLENBOGEN B.S.;

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RL	J. BIOL. CHEM.	267;9868-9873(1992).
RP	VARIANT CYS-160.	
RA	ANDERSEN T.I., WOOSTER R., LAKE K., COLLINS N., WARREN W., SKREDE M.,	
RA	EELDES R., TWIT K.M., JOHNSTON S.R.D., DOWSETT M., OLSEN A.O.,	
RA	MOELLER P., STRATTON M.R., BOERRESSEN-DALE A.-L.;	
RL	HUM. MUTAT. 9:531-536(1997).	
CC	-I- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN	
CC	THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR	
CC	PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.	
CC	-I- SUBUNIT: HOMODIMER.	
CC	-I- SUBCELLULAR LOCATION: NUCLEAR.	
CC	-I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,	
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	
CC	-I- IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT	
CC	TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS. HORMONE BINDING	
CC	GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR	
CC	COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF	
CC	TRANSCRIPTIONAL START SITES.	
CC	-I- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC	
CC	NUCLEAR HORMONE RECEPTORS.	
DR	EMBL; X03635; G31234; -.	
DR	EMBL; M12674; G182193; -.	
DR	PIR; A03244; QRHUE.	
DR	HSSP; P06536; 1GDC.	
DR	TRANSFAC; T00261; -.	
DR	MIM; I33430; -.	
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.	
KW	RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;	
KM	ZINC-FINGER; STEROID-BINDING; POLYMORPHISM.	
FT	DOMAIN	1 184
FT	DNA_BIND	185 250
FT	ZN_FING	185 205
FT	ZN_FING	221 245
FT	DOMAIN	251 310
FT	DOMAIN	311 551
FT	STEROID-BINDING.	160 160
FT	VARIANT	400 400
FT	G -> V (DESTABILIZES THE RECEPTOR AND	
FT	DECREASES ITS AFFINITY FOR ESTRADIOL AT	
FT	25 DEGREES CELSIUS, BUT NOT AT 4 DEGREES	
FT	CELSIUS).	
FT	C -> A (LOSS OF HORMONE BINDING CAPACITY	
FT	AND TEMPERATURE-SENSITIVE LOSS IN DNA-	
FT	BINDING).	
EQ	SEQUENCE	595 AA; 66216 MW; D6945BB9 CRC32;
SQ	Query Match	43.4%; Score 1693; DB 1; Length 595;
	Best Local Similarity	56.8%; Pred. NO. 0.00e+00;
	Matches	229; Conservative 98; Mismatches 59; Indels 17; Gaps 13
Db	178 SAKETRYCAVNCNDASGYHYGVSCSECGKAFFKRSIQGHNDYMCPRAINOCITDKNRKSC	237
Qy	142 SKRDHFCAVCSDYASGHHYGVSCGCKAFKKRSIQGHNDYICPAINOCITDKNRKSC	201
Db	238 QACRIARKCYEGMMKGGRKDRRGRRMKHKHRDDGGREGVEVSAGDMRAANTMPSPLM	297
Qy	202 QACRIARKCYEGMMKCGSRERRRCYRIIV--RQSADN-QIHCKGKA-KRSGG--NAP-R	254
Db	298 IKRSKNLSLALSLADQNVAYLLDAEPP-IlySEYDTPRPFSSEASMGLLTNLINADRELVI	356
Qy	255 V-RELL-ID-ALSPQLVLTLLEAEPPHVLIISR--PSAPTSAEMMSSTKLADKIELVI	308
Db	357 MINNAKRYPGVVDLTLDHQVILLLECAMELTMIGLVWRSMHPKFLFAPRYLLDDRNGK	416
Qy	309 MISMAKKIRPGVEVSLTFQVRHLSCWMEVLMGMWSIDHPKLFAPRVLDLRDEGK	368
Db	417 CVEGWEVFEDMLILTSSRFPMNSLOGEFVPLKSIILINSGVYFLSTSLKSEKHIIH	476
Qy	369 CVEGLELTFMDLMTATSFRRELKIQHKKYLCLVKAMILLNSSMYLVATAQDA-DSSRKLA	427
Db	477 RVLDKIITDTLLHAAKAGLTQQOHRLAQLLLISHTIRKSNKGMEHLYSMACKNYVPL	536
Qy	428 HLINLVATLVAVIKASSISSOSMRANLIMLISHVFAHSNKGMEHLLMMCKNNVPV	487

Db 537 YDLLEMLDAHRLHA-PTSRGASVEETDQSLATAGSTSSHS 578
 488 YDLLEMLNAHVLRGCKSSITGSECSPAEDSK-SKEGSONPOS 529

RESULT 3
 ID ESTR_MOUSE STANDARD: PRT: 599 AA.

AC P19785;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR).
 GN ESR1 OR ESR OR ESTR OR ESTRA.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 EUTHERIA; RODENTIA.

[1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-UTERUS;
 RX MEDLINE; 91042558.
 RA WHITE R., LEES J.A., NEEDHAM M., HAM J., PARKER M.;
 RL MOL. ENDOCRINOL. 1:735-744(1987).

-1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 -1- SUBUNIT: HOMODIMER.
 -1- SUBCELLULAR LOCATION: NUCLEAR.
 -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 -1- IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.
 -1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC ACID NUCLEAR HORMONE RECEPTORS.

EMBL; M38651; G193180; -;
 DR PIR; A40061; A40061.
 DR HSSP; P06536; 1GDC.
 DR TRANSFAC; T00259; -;
 DR MGD; MGI:109348; ESTRA.
 DR PROSITE; P500031; NUCLEAR_RECEPTOR; 1.
 KW RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 FT ZINC-FINGER; STEROID-BINDING.
 FT DOMAIN 1 188
 FT DNA_BIND 189 254
 FT ZN_FING 189 209
 FT ZN_FING 225 249
 FT DOMAIN 255 599
 FT DOMAIN 64 72
 FT SEQUENCE 599 AA; 66955 MW; 6ED9EAD6 CRC32;

Query Match 42.8%; Score 1669; DB 1; Length 599;
 Best Local Similarity 51.7%; Pred. No. 0.00e+00;
 Matches 246; Conservative 106; Mismatches 104; Indels 20; Gaps 14;

Db 108 SPSPLMLHPPLPOLSPFLPHGQVYIENESAT-AVRDTPPAPFYNSNSNRQNGR 166
 73 TTSPLYLWPTPGLSP-LVYHRLSLHYAEPKSPWCARSLEHTLPVNRKTLKRVSG- 130

Db 167 ERLSSNEKGMIMESAKETRYCAVNDYASGYHYWSEGCAPFKRSIOGHNDYMP 226
 131 NR-CASPVYGP---GSKRAHCAVSDYASGYHYWSEGCAPFKRSIOGHNDYICD 186

Db 227 AINQCTIDNRKRSQACRLRKCYEGVMKGGIRKDRGRMLKHKRRDDLEGRNEMGA 286
 187 AINQCTIDNRKRSQACRLRKCYEGVMKGGIRKDRGRMLKHKRRDDLEGRNEMGA 286

Db 287 SGDMRANLMPSPLYIKHKTKNSPALSLADQVYSALDLAEPMTIYSEIDPSRPESEAS 346
 243 GAKRSGG--HARV-RELLD--ALS--PEOLVTLLEAEPHVLIS-RPSAPFTEASM 294

Db 347 MGLINLADRELHYMINMAKRVPGFDNLHDQVHLLCEAMLEILMIGLVRSMEHPGRL 406
 295 MSLTKLADRELHYMINMAKRTIPGEVLSLPDQVRLLESCWMEVLMGLMWSIDHPRLL 354

Db 407 LPARNLLDRNOCKCYEGNVEIFDMILATSSRRMMNLOGEEFVCLKSTILLNSGYTTL 466
 355 IFAPDLVLRDECKCYEGVLEIFDMILATSSRRREKLKHQKECYKAMILLNSSMYPLV 414

Db 467 SSTLSLEEKDHHRVLDKITDPLIHLMAKAGITLQOQHRLAQLLLIISHTRHMSNKG 526
 415 TATQDA-DSSRLAHLLNVTDLVWVIAKSGISSQOQSMRLANLVLHVRHASNKG 473

Db 527 EHLNKKCRNVPLYDLLEMLDAHRLHAPASRMGPPEPQOTLATTSTSAHS 582
 474 EHLNKKCRNVPLYDLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPOS 529

RESULT 4
 ID ESTR_RAT STANDARD: PRT: 600 AA.

AC P06211;
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR).
 GN ESR1 OR ESR OR ESTR.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 EUTHERIA; RODENTIA.

[1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR;
 RA MURAMATSU M.;
 RL SUBMITTED (MAR-1987) TO EMBL/GENBANK/DBJ DATA BANKS.

[2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87174780.
 RA KOIKE S., SAKAI M.;
 RL NUCLEIC ACIDS RES. 15:2499-2513(1987).

[3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-UTERUS;
 RA MAGGI A.M.A.;
 RL SUBMITTED (JUN-1991) TO EMBL/GENBANK/DBJ DATA BANKS.

-1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 -1- SUBUNIT: HOMODIMER.
 -1- SUBCELLULAR LOCATION: NUCLEAR.
 -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 -1- IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.
 -1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC ACID NUCLEAR HORMONE RECEPTORS.

EMBL; Y00102; G56111; -;
 DR EMBL; X61098; G56121; -;
 DR PIR; S07379; S07379.
 DR HSSP; P06536; 1GDC.
 DR TRANSFAC; T00258; -;
 DR PROSITE; P500031; NUCLEAR_RECEPTOR; 1.
 KW RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 FT ZINC-FINGER; STEROID-BINDING.
 FT DOMAIN 1 189
 FT DNA_BIND 190 255
 FT ZN_FING 190 210
 FT ZN_FING 226 250
 FT ZN_FING 226 250
 FT DOMAIN 256 600
 FT DOMAIN 64 71
 FT SEQUENCE 600 AA; 67030 MW; 4CC59B2 CRC32;


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CC      A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC      -1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC      NUCLEAR HORMONE RECEPTORS.
DR      EMBL: 265555; E212241; -.
DR      PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
KW      RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KM      ZINC-FINGER; STEROID-BINDING.
FT      NON_TER      1      1
FT      DOMAIN      <1      15      MODULATING, PRO-RICH.
FT      DNA_BIND      18      83      C4-TYPE ZINC FINGERS (TWO).
FT      ZN_FING      18      38      C4-TYPE.
FT      ZN_FING      54      78      C4-TYPE.
FT      DOMAIN      128      377      STEROID-BINDING.
FT      NON_TER      377      377
SQ      SEQUENCE      377 AA; 42840 MW; 6F0DD900 CRC32;

Query Match      17.4%; Score 679; DB 1; Length 377;
Best Local Similarity 34.6%; Pred. No. 5,25e-130;
Matches 102; Conservative 82; Mismatches 98; Indels 13; Gaps 13;

DB      17      ICILGDEASGCHYVLTGSCVYFKRAMEGQHNYLCAGRNDCTVDKRRKNCPCRLR 76
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      148      FCAYCSDYASGYHGVWSCGCKAFKRSIQGHNDYICPATNCTIDKNRKSQACRLR 207
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      77      KCCQAGVYL-GGRKFK-KFNKVRMRTLDVALPQVGINESQALSQRTFSSQDLQ 134
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      208      KCYEVGAVKCGSRRCRGYLRVRRGSADE-QL-HCAGKAKRSGGHPVRV-ELLDD-AL 263
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      135      IP-PLINLMSIEPDVYAGHDNKSPTSSSLTSLNOLGERQLLSVYKMSKLPGRNL 193
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      264      SPEDVLVTLLEAPPHVLISRPSA-PPTASMMMSLTKLADKELVHMISSAKKIPGVEL 322
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      194      HIDDQITLIQYSWMSLVFGLGWSYKSGQMLYFAPDLILNQRMK-ESSFYSLCLTM 252
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      323      SLDPQVRLSCWMEVLMGLMRSIDH-PGKLI-FAPDLVLDDECKVEGILFIDML 380
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      253      WQIPQEVKIQVSEEFELCKVLLLTITPLEGLRSQNGEEMSSITQILIKAI 307
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      381      LATTSRRELKLOHKEYLCVAMILLNS-SMYPVLTATQ-DADSSRLAILNLAV 433

RESULT 13
ID      PRGR_MOUSE      STANDARD;      PRT;      923 AA.
AC      000175;
DT      01-DEC-1992 (REL. 24, CREATED)
DT      01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DE      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      PROGESTERONE RECEPTOR (PR).
GN      PGR OR PR.
OS      MUS MUSCULUS (MOUSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; RODENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 91299759.
RA      SCHOTT D.R., SHYAMALA G., SCHNEIDER W., PARRY G.;
RL      BIOCHEMISTRY 30:7014-7020(1991).
RN      [2]
RP      SEQUENCE OF 1-9 FROM N.A.
RX      STRAIN-129/SV.
RX      MEDLINE; 95100931.
RA      HAGIHARA K., WO-PENG X.S., FUNABASHI T., KATO J., PRAFF D.W.;
RL      BIOCHEM. BIOPHYS. RES. COMMUN. 205:1093-1101(1994).
CC      -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC      THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC      PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC      -1- SUBCELLULAR LOCATION: NUCLEAR.
CC      -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC      A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC      -1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC      NUCLEAR HORMONE RECEPTORS.
DR      EMBL: M68915; G200472; -.
DR      EMBL: U12644; G639917; -.

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DR      PIR: A39596; A39596.
DR      HSP; P06536; 1GDC.
DR      MGD; MGI:97567; PGR.
DR      PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
KW      RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KM      ZINC-FINGER; STEROID-BINDING.
FT      DOMAIN      1      556      MODULATING, PRO-RICH.
FT      DNA_BIND      557      622      C4-TYPE ZINC FINGERS (TWO).
FT      ZN_FING      557      577      C4-TYPE.
FT      ZN_FING      593      617      C4-TYPE.
FT      DOMAIN      671      923      STEROID-BINDING.
FT      DOMAIN      184      188      NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ      SEQUENCE      923 AA; 99073 MW; EEDPFA1A CRC32;

Query Match      17.4%; Score 681; DB 1; Length 923;
Best Local Similarity 30.8%; Pred. No. 1.69e-130;
Matches 123; Conservative 112; Mismatches 138; Indels 27; Gaps 27;

DB      491      AAGTAAAPAIYPLG-LNGLPQIG-Y-QANVAKDSLPOYPPYLYLTPRDSASQSPQ 547
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      81      PTEGHLSPVLVHRQLSHLAEQKSPWCERSLSLEHTLP-VNRETLK-RKVSGRCASPYT 138
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      548      GFDSPLO-KICILGDEASGCHYVLTGSCVYFKRAMEGQHNYLCAGRNDCTVDKRR 606
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      139      GPGSKDAHFCAVCSYASGYHGVWSCGCKAFKRSIQGHNDYICPATNCTIDKNR 198
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      607      KNCPCRLKCCQAGVYL-GGRKFK-KFNKVRMRTLDVALPQVGLPNESQALSQRT 664
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      199      KSCQACRLKRCYGVAVKCGSRRCRGYLRVRRGSADE-QL-HCAGKAKRSGGHPVRV 256
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      665      FSNQELQVLP-PLINLMSIEPDVYAGHDNKSPTSSSLTSLNOLGERQLLSVYKMS 723
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      257      ELLDPA-SPEDVLVTLLEAPPHVLISRPSA-PPTASMMMSLTKLADKELVHMISSA 313
DB      724      KSLPGRNLHIDDQITLIQYSWMSLVFGLGWSYKSGQMLYFAPDLILN-EG-R-MK 780
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      314      KKIPIGVEVSLFQVRLSCWMEVLMGLMRSIDH-PGKLI-FAPDLVLDDECKVE 371
DB      781      E-LSFYSLCLTMQIPOEFVKLVTHEEFELCKVLLLTNT-I-PLGLRSQSQFEEMRS 837
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      372      GILEIFDM-L-L-ATTSRRELKLOHKEYLCVAMILLNS-SMYPVLTATQDADSSRLKLN 428
DB      838      YIRELIKAIIG-LRQKGVNTPSQRFYQTLKLDLSLHVLNQ 876
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      429      LLNAVTDALWVYAKSGISSQOQSMRLANL-LTSLSHVSH 467

RESULT 14
ID      PRGR_HUMAN      STANDARD;      PRT;      933 AA.
AC      P06401;
DT      01-JAN-1988 (REL. 06, CREATED)
DT      01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DE      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      PROGESTERONE RECEPTOR (PR).
GN      PGR.
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PRIMATES.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 90228361.
RA      KASTNER P., KRUST A., TURCOTTE B., STROPP U., TORA L., GRONEMEYER H.,
RA      CHAMON P.;
RL      EMBO J. 9:1603-1614(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 87184565.
RA      MISRAHI M., ATGER M., D'AURIOL L., LOOSFELT H., MERIEL C.,
RA      FRIDLANDSKY F., GUTCHON-MANTEL A., GALIBERT F., MILGROM E.;
RL      BIOCHEM. BIOPHYS. RES. COMMUN. 143:740-748(1987).
CC      -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC      THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC      PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

```


CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- ALTERNATIVE PRODUCTS: THERE ARE TWO FORMS OF THE PROGESTERONE
CC RECEPTOR: FORM A (THAT STARTS WITH MET-1) AND FORM B (THAT STARTS
CC WITH MET-165).
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC NUCLEAR HORMONE RECEPTORS.
DR EMBL: X51730; G35652; -.
DR EMBL: M15716; G189935; -.
DR PIR: A03245; ORHDP.
DR PIR: S09971; S09971.
DR HSP: P06536; IGDC.
DR TRANSFAC: T00696; -.
DR MIM: 264080; -.
DR PROSITE: PS00031; NUCLEAR RECEPTOR: 1.
DR RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW ZINC-FINGER; STEROID-BINDING; PHOSPHORYLATION; ALTERNATIVE SPLICING.
FT DOMAIN 1 566
FT DNA_BIND 567 632
FT ZN_FING 567 587
FT ZN_FING 603 627
FT DOMAIN 681 933
FT MOD_RES 183 187
FT MOD_RES 41 41
FT MOD_RES 227 227
FT MOD_RES 232 232
FT MOD_RES 552 552
FT MOD_RES 793 793
FT VARSLIC 1 164
FT CONFLICT 226 226
FT CONFLICT 256 256
FT CONFLICT 344 344
FT CONFLICT 660 660
SQ SEQUENCE 933 AA; 99042 MW; 0D1124EB CRC32;
Query Match 17.1%; Score 666; DB 1; Length 933;
Best Local Similarity 33.4%; Pred. No. 8.35e-127;
Matches 110; Conservative 89; Mismatches 113; Indels 17; Gaps 17;
Db 566 ICILICDEASGCHYGVLTGSCVFFFRAMEGQHNYLCAGRNDICVDKIRKNCPCACRLR 625
Qy 148 FCVAVCSDYASGYHYWSCGCAFFKRSIQGNDYICATNOCITDKNKRKSCQACRLR 207
Db 626 KCCQAGNVL-GGRKFK-KENKVRVNRALDAVALPQVIGVNSQALPRTSPSOEIQ-LIP 662
Qy 208 KCYEVMVWCGSRRCRGYLVRRORSAD-QL-HCAGKAKRSRGHAPRVRELLDALSP 265
Db 684 IP-PLINLMSIEPVIYAGHDNTPDSSSLTSLNQLGEROLLVYKMSKSLPFRNL 742
Qy 264 SPQVLTLLEAPPHVILSRSA-PFTESMMSLTKLADKELVHMSAKKIPGVVEL 322
Db 743 HIDDITLLOYSMWSLWFGWRSYKRVSGQMLYFADPDLINLQRMK-ESSFYSICLTLMQ 801
Qy 323 SLFDQVRLLESCEMVEYLMGLMWSIDH-PGKLI-FAPDLVLDREDEKCEVEGILEIFDML 380
Db 802 WQIPQEFVKLOVSOEFLCMVLLNTIPLEGRSOTO-FEEMRS-SYI-RELIRAIQ- 857
Qy 381 LATTSFRELKLOHKEYLCVAMILLNS-SMYPVATATDADSSRLAHLLNAVTDALVW 439
Db 858 LROGVVSSQRFYQTLTKLDNLHDLVKQ 886
Qy 440 VIKSGISSQOSMRLANLL-MLSHYRH 467
RESULT 15
ID PRGR_RABIT STANDARD; PRT; 930 AA.
AC P06186;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PROGESTERONE RECEPTOR (PR).
GN

OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; LAGOMORPHA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 87067449.
RA LOOSELY F., ANGER M., MISRAHI M., GUIOCHON-MANTEL A., MERIEL C.,
RL LOGEAT F., BENAROUS R., MILGROM E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:9045-9049(1986).
CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC NUCLEAR HORMONE RECEPTORS.
DR EMBL: M14547; G165632; -.
DR PIR: A25923; A25923.
DR HSP: P06536; IGDC.
DR TRANSFAC: T00697; -.
DR PROSITE: PS00031; NUCLEAR RECEPTOR: 1.
DR RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW ZINC-FINGER; STEROID-BINDING.
FT DOMAIN 1 565
FT DNA_BIND 566 633
FT ZN_FING 566 588
FT ZN_FING 604 628
FT ZN_FING 678 930
FT DOMAIN 184 188
SQ SEQUENCE 930 AA; 98666 MW; EE133E86 CRC32;
Query Match 17.0%; Score 662; DB 1; Length 930;
Best Local Similarity 32.5%; Pred. No. 8.05e-126;
Matches 106; Conservative 91; Mismatches 114; Indels 15; Gaps 15;
Db 567 ICILICDEASGCHYGVLTGSCVFFFRAMEGQHNYLCAGRNDICVDKIRKNCPCACRLR 626
Qy 148 FCVAVCSDYASGYHYWSCGCAFFKRSIQGNDYICATNOCITDKNKRKSCQACRLR 207
Db 627 KCCQAGNVL-GGRKFK-KENKVRVNRALDAVALPQVIGVNSQ-LIP 662
Qy 208 KCYEVMVWCGSRRCRGYLVRRORSAD-QL-HCAGKAKRSRGHAPRVRELLDALSP 265
Db 683 -PLINLMSIEPVIYAGHDNTPDSSSLTSLNQLGEROLLVYKMSKSLPFRNLH 741
Qy 266 EQVLTLLEAPPHVILSRSA-PFTESMMSLTKLADKELVHMSAKKIPGVVELSL 324
Db 742 DDQITLLOYSMWSLWFGWRSYKRVSGQMLYFADPDLINLQRMK-ESSFYSICLTLMQ 800
Qy 325 FQVYRLLESCEMVEYLMGLMWSIDH-PGKLI-FAPDLVLDREDEKCEVEGILEIFDMLA 382
Db 801 IPOEFVKLOVSOEFLCMVLLNTIPLEGRSOTO-FEEMRS-SYI-RELIRAIQ-LRQ 857
Qy 383 TTSFRELKLOHKEYLCVAMILLNS-SMYPVATATDADSSRLAHLLNAVTDALVWYA 442
Db 858 KGVVSSQRFYQTLTKLDNLHDLVKQ 883
Qy 443 KSGISSQOSMRLANLL-MLSHYRH 467
Search completed: Mon Nov 2 16:32:02 1998
Job time : 57 secs.

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Db	2545	AAGCTGCGCATGCT	2557
Qy	725	aagtgcgaatcgt	737

RESULT	5
ID	US-08-260-452-8 STANDARD; DNA; UNC; 6244 BP
AC	xxxxxx

DE Sequence 8, Application US/08260452
CC Sequence 8, Application US/08260452
CC Patent No. 5650298
CC
CC GENERAL INFORMATION:
CC APPLICANT: Gossen, Manfred
CC APPLICANT: Bujard, Hermann
CC APPLICANT: Salfeld, Jochen
CC APPLICANT: Voss, Jeffrey
CC TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotid
CC TITLE OF INVENTION: Cells by Tetracycline-responsive Promoters
CC NUMBER OF SEQUENCES: 10
CC
CC CORRESPONDENCE ADDRESSES: 10

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CC COMPUTER READABLE FORM: disk
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: ASCII text
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/260,452
CC FILING DATE:
```

CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/076,327
CC ATTORNEY/AGENT INFORMATION:
CC NAME: GIULIO A. DECONTI, J.
CC REGISTRATION NUMBER: 31,503
CC REFERENCE/DOCKET NUMBER: BPI-013C3C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 227-7400
CC TELEFAX: (617) 227-5941
CC INFORMATION FOR SEQ ID NO: 8:

Query Match	3.78;	Score 63;	DB 1;	Length 6244;
Best Local Similarity	66.3%;	Pred. No. 3.17e-29;		
Matches 128:	Conservative	0;	Mismatches 65;	Indels 0;
				Gaps 0;

Db	Qy	Db	Qy
2365	TCGTGGGGGATGAAGCACTCAGGCGTGTATTATGGTCTGTCACACTGTGGAGCTGTGAAG	2424	TCGTGGGGGATGAAGCACTCAGGCGTGTATTATGGTCTGTCACACTGTGGAGCTGTGAAG
545	ttctgaagcagattacgacatcgagatactcaactcagtagctgctgtgtgaagatgtaag	604	ttctgaagcagattacgacatcgagatactcaactcagtagctgctgtgtgaagatgtaag
2425	TCTTCTTTAAAAGGCATGGAAGGCGACGATACCTTTATATGCTGGGAGAAATGACT	2488	TCTTCTTTAAAAGGCATGGAAGGCGACGATACCTTTATATGCTGGGAGAAATGACT
605	ccctttcttaaaagagccttcaagacataatgattatatttccagctacacacagtt	664	ccctttcttaaaagagccttcaagacataatgattatatttccagctacacacagtt

Db 2485 GCATTGTTGATTAATTAACCCGAGAGAAAATGCGCCGCGGTGCTTGAAGAATGCTCTC 2544
 665 gtacaatcagataaaccgcggcgcaagagctgcaggcctgcgaacttcggaagtgtaacg 724
Qy 2545 AAGCTGGCATTGCT 2557
 725 aagtcggaaatcgtg 737
Db

RESULT	6
ID	US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP
AC	xxxxxx

DE	Sequence 14, Application	US/08232463
CC	Sequence 14, Application	US/08232463
CC	Patent No. 5670367	
CC	GENERAL INFORMATION:	

CC APPLICANT: DORNER, F.
CC APPLICANT: SCHEIFLINGER, F.
CC APPLICANT: FALKNER, F. G.
CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC NUMBER OF SEQUENCES: 52
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 100 Diagonal Road, Suite 500
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/232,463
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/935,313
CC

CC FILING DATE: EP 91 114 300.6
CC APPLICATION NUMBER: 26-AUG-1991
CC FILING DATE: 26-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BENT, Stephen A.
CC REGISTRATION NUMBER: 29,768
CC REFERENCE/DOCKET NUMBER: 30472/114 IMM
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703)856-8300
CC TELEFAX: (703)683-4109
CC TELEFAX: 899149

Query Match	3.7%;	Score 62;	DB 1;	Length 7218;
Best Local Similarity	1.4%;	Pred. No. 1.82e-28;		
Matches	5;	Conservative	205;	Mismatches 148;
			Indels	0;
			Gaps	0;

[illegible]

Qy	656	caatcagttgtaacatcgataaaacccggcgcaagagctgcgcagctgcgcgaattcgsa	715
Db	367	AATGTCCTTCAGGCTGAATG	386
Qy	716	agtyrtacgaagtgggaatg	735

RESULT	14
ID	PCT-US92-02320A-3 STANDARD; DNA; UNC; 2928 BP
AC	xxxxxx

DE Sequence 3, Application PC/TUS9202330A
DE Sequence 3, Application PC/TUS9202330A
CC GENERAL INFORMATION:
CC APPLICANT: Sloan-Kettering Institute, For Cancer Research
CC TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: COOPER & DUNHAM
CC STREET: 30 ROCKEFELLER PLAZA
CC CITY: NEW YORK
CC STATE: NEW YORK
CC COUNTRY: U.S.A.
CC ZIP: 10112
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.24
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/02320A
CC FILING DATE:

Query Match	2.58;	Score 42;	DB 2;	Length 2928;
Best Local Similarity	60.68;	Pred. No. 8.39e-14;		
Matches 120: Conservative	0;	Mismatches 78;	Indels 0;	Gaps 0

[illegible]

QY	598	tgttaagggcctttttaaagaagacatccaagacatatgatatttgcgcgcaca	657
Db	484	AAGAATGCATCATCAACAAGAGGTATCCCGAATCCGCTAGTACTCCATCTGCACAG	543
QY	658	aatacagtgtaacaatcgtataaaacaacgcgcgaagctgcgcgaagctgcgcgaattcgaag	717
Db	544	TGCTTTGAAGTGGGCATG	561
QY	718	tgttacgaagtcgggaatcg	735

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RESULT 15
ID 5171671-1 STANDARD; DNA; UNC; 3185 BP.
AC xxxxxx
DE 01-JAN-1900
DE Patent No. 5171671.
CC Patent No. 5171671
CC APPLICANT: EVANS, RONALD M.;ONG, ESTELLE S.;SEGUI,
CC PRUD'HMAR S.;THOMPSON, CATHERINE C.;UMESONO, KAUUHIKO
CC GUGIERE, VINCENT
CC TITLE OF INVENTION: RETINOIC ACID RECEPTOR COMPOSITION
CC NUMBER OF SEQUENCES: 2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/546,256
CC FILING DATE: 06-AUG-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 276,536
CC FILING DATE: 30-NOV-1988
CC APPLICATION NUMBER: 128,331
CC FILING DATE: 02-DEC-1987
CC SEQ ID NO:1:
CC LENGTH: 2940
SQ Sequence 3185 BP: 594 A; 1010 C; 790 G; 546 T; 245 other;

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	Query Match	2.5%;	Score 42;	DB 3;	Length 2940;
	Best Local Similarity	60.6%;	Pred. No. 8,39e-14;		
	Matches 120;	Conservative	0;	Mismatches 78;	Indels 0; Gaps 0;
Db	364	TGCTTTGTCTGTACGACAGACTCTCAGGCTACCATATGGGGTCAGCGCTGTGAGGC	423		
Qy	538	tgcgcgtgctgcagcgatcagcactcgysatatacactatgagctgtgctgtgaaaga	597		
Db	424	TGCAAGGGCTCTTCCTCCGCCAGATCCAGAAACAATGGTGTCACAGGTGCACCGGAC	483		
Qy	558	tgttaagagccctttttaagaagaacatccaagaacataatgtattatlttccagctaca	657		
Db	484	AAGAACTGCATATCATCAACAGAGTATACCCGGAAACGCTGCCAGTACTGCCGACTGCAGAG	543		
Qy	658	aatcagctgtacaatcagataaacaacccgycgaagctgtccagcgtccgagcttcggaag	717		
Db	544	TGCTTTGAAGTGGGGCAT 561			
Qy	718	tgttacgaagctgggaatg 735			

Search completed: Tue Nov 3 04:58:08 1998
Job time : 79 secs.

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GSECPADSKSBSGONPOSO*
BASE COUNT 425 a 463 c 459 g 393 t
ORIGIN

Query Match 99.9%; Score 1684; DB 21; Length 1740;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1685; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 CAGCCATTACTTGGCCAGATCTTTGAGAACATTAATGACCTTTGCTCTTCT 65
QY 1 cagccattacttggccagatctttgagaaacattatgaccttggctcttct 60
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QY 61 tgcgaagtggttttcagctgttatctcaagacatgagataaaaaaccacacatcagc 120
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QY 121 cttaatctcctctcctcccaacatgcaatccatcttaacctggagcaagctcc 180
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QY 181 atatacatcttctcctctatgtagacagccacatgaaatccatcagcatgacattcat 240
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QY 241 agccctgctgtatgattaatacagcattccagaaatgtacatcttgaagtgagct 300
Db 306 GGTGCGACACACCAAGCCCAATGTGTGTGGCCAACTGGGCACTTCTCTCTTTA 365
QY 301 ggtgcgacacacccaagcccaatgtgtgtggccaaactgggcaacttctctttaa 360
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QY 361 gtgtgtcatgctgcatattacatcgtatgcygaacccaagaagtgctgtgtga 420
Db 426 GCAGATGCTGTAGAACACCTTACTGTAAGAGAGACATGTAAGAGAGGTATG 485
QY 421 gcaagatcgttagaacaacatcctgtaaaagagagacactgaaagagagtgatg 480
Db 486 GGGAGCCGTTGGCCGACCTGTACTGTGCTCAGGTCAAGGAGGATGCTCACTCTCG 545
QY 481 gggagccgttggccgacccctgttactgtgccaaggttcaagagagtgatcttcgc 540
Db 546 GCTGTGTGACGAGATTACGATCGGATATCACTATGAGTGTGTGTGTGAAGATGT 605
QY 541 gctgtgtgacgagattacgcatcgagatacctatgagtgctgtgtgtgaagatgt 600
Db 606 AAGGCTTTTAAAGAACATTTCAAGGACATATGATATATTTGTCAGCTTACAAT 665
QY 601 aaggctttttaaagaacatcattcaaggaacataatgattatctgtccaagctacaat 660
Db 666 CAGTGTACATCGATAAATCCGCGCAGAGAGTGGCAGGCTGCGCACTTGGAAATGT 725
QY 661 cagtgtacaatcgataaaaaacgagcaagagctgccaagccctgcgaacttggaggt 720
Db 726 TACGAAGTGGGAATGCTGAAGTGTGCTCCGAGAGAGAGATGTGGATCCGCTTGTG 785
QY 721 tacgaagtgggaatgctgaagtgtgctcccgagagagagatggtggtacgcctgtg 780
Db 786 CGAGAGACAGAGAGTGGCGAGAGACATGCTGCTGCGGCAAGGCAAGAGAGTGGC 845
QY 781 cggagagagagagagtgccgagagcagctgacatgctgagcgaagcaagaagaagtg 840
Db 846 GGGCAGCGCGCCGAGATGCGGAGCTGCTGTGACGCCCTGAGCCCGAGAGCTAGTG 905
QY 841 gggcagcgccgagatgctgagctgtgtgtgagcagccctgagcccgagcagctagtg 900
Db 906 CTCACCTCTCTGAGGCTGAGCGCCGCCCATGTGCTGATCAGCGCCCACTGGCCCTTC 965

QY 901 ctcacccctcgagagctgagccgcccaatgtgtgtatcagccgccagtgcccttc 960
Db 966 ACCGAGGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1025
QY 961 accgagggctccatgagatgagtgatgagtgatgagtgatgagtgatgagtgatgag 1020
Db 1026 ATCAGCTGGGCGCAAGAGATTCGCGGCTTTGTGAGCTCAGCTGTTGCACCAAGTCCG 1085
QY 1021 atcagctggcgcaagagatgagtgatgagtgatgagtgatgagtgatgagtgatgag 1080
Db 1086 CTTTGGAGAGCTGTGTGATGAGAGTGTATGATGAGGCTGATGAGTGGCTGATGATGAC 1145
QY 1081 ctcttgagagctgtgtgagtgagtgatgagtgatgagtgatgagtgatgagtgatgag 1140
Db 1146 CACCCGCGCAAGCTATGCTGCTCAGAGATGCTGTTGTCGACAGGAGATGAGGGAATGC 1205
QY 1141 caaccgagagctccatcttggctccagatctgtcttgagcaagagatgagtgagtgag 1200
Db 1206 GTAGAGAGATTTGGAATCTTGTGACATGCTCTGCACTACTTCAAGTTTCAGAG 1265
QY 1201 gtagagagatcttggaatcttgacatgctcttgcaactacttcaagtttcgagag 1260
Db 1266 TTAACCTCCAAACAAAGATATCTGTGTGCAAGGCAATGATCTGCTCAATTCAGT 1325
QY 1261 ttaaacctccaaacaaagatattctgtgtgcaagcaagatctgctcaatccag 1320
Db 1326 ATGTACCTCTGTGTCACAGCAGCCAGAGCTGTGACAGCAGCCGGAAGCTGCTACTTG 1385
QY 1321 atgtacctctgtgtacagcgagccagagatgtgtgacagcgagagctgtccactg 1380
Db 1386 CTGAAGCCCGTACCGATGCTGTTGTTGGTGTATGTCGAAGAGCGGATCTCTCCAG 1445
QY 1381 ctgaagcccgtagccgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
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QY 1441 cagcaatcagtcgctgt 1500
Db 1506 AACAGGCGCATGGAATCTGCTCAACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1565
QY 1501 aacaaggcgatgagacatctgtcaacatgagtgagtgagtgagtgagtgagtgagtg 1560
Db 1566 CTGTGCTGTGAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1625
QY 1561 ctgtgctgtgagatctgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1620
Db 1626 TCCGAGTGCAGCGCGGAGAGAGAGTAAAGCAAGAGGCTCCAGAACCCAGAGCT 1685
QY 1621 tcgagtgagcgccgag 1680
Db 1686 CAGTGA 1691
QY 1681 cagtga 1686

RESULT 2
LOCUS AF051427 2011 bp mRNA PRI 19-MAR-1998
DEFINITION Homo sapiens estrogen receptor beta mRNA, complete cds.
ACCESSION AF051427
NID 92970563
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2011) Moore, J.T., McKee, D.D., Moore, L.B., Jones, S.A., Su, J.-L.,
AUTHORS Slentz-Kesler, K., Horne, E.L., Klierer, S.A., Lehmann, J.M. and
TITLE Cloning, Ligand Binding and Functional Activity of Human Estrogen
Receptor beta Isoforms
JOURNAL Unpublished

Db 2007 AGTGA 2011
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QY 1682 agtga 1686

RESULT 3
LOCUS AF051428 2041 bp mRNA PRI 17-MAR-1998
DEFINITION Homo sapiens estrogen receptor beta2 splice variant mRNA, complete cds.
ACCESSION AF051428
NID 92961558
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2041)
AUTHORS Moore, J.T., McKee, D.D., Moore, L.B., Jones, S.A., Su, J.-L.,
Horne, E.L., Klierer, S.A., Lehmann, J.M. and Willson, T.M.
TITLE Cloning, Ligand Binding and Functional Activity of human Estrogen
Receptor beta Isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2041)
AUTHORS Moore, J.T., McKee, D.D., Moore, L.B., Jones, S.A., Su, J.-L.,
Horne, E.L., Klierer, S.A., Lehmann, J.M. and Willson, T.M.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1998) Molecular Sciences, Glaxo Wellcome, 5 Moore
Drive, RTP, NC 27709, USA

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RESULT 5 AB006589 3593 bp mRNA PRI 28-JUL-1998
LOCUS Homo sapiens mRNA for estrogen receptor beta cx, complete cds.
DEFINITION
ACCESSION AB006589
NID 93345671
KEYWORDS estrogen receptor beta cx.
SOURCE Homo sapiens CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Ogawa,S., Inoue,S., Watanabe,T., Orimo,A., Hosoi,T., Ouchi,Y. and
Muraiatsu,M.
TITLE Molecular cloning and characterization of human estrogen receptor
beta cx: a potential inhibitor of estrogen action in human
Nucleic Acids Res. 26, 3505-3512 (1998)
2 (bases 1 to 3593)
Ogawa,S.
Direct Submission
Submitted (13-AUG-1997) to the DDBJ/EMBL/GenBank databases. Sumito
Ogawa, Saitama Medical School, Department of 2nd Biochemistry; 38
Morohongo, Moroyama, Iruma-gun, Saitama 350-0495, Japan
(E-mail:suogawa@saitama-med.ac.jp, Tel:81-492-76-1490,
Fax:81-492-94-9751)

FEATURES
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NI	el262494		
DT	09-MAR-1998 (Rel. 54, Created)		
DT	09-MAR-1998 (Rel. 54, Last updated, Version 0)		
DE	Sequence 4 from Patent WO9709348.		
NC	Homo sapiens (human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;		
CC	Cararrhini; Homnidae; Homo.		
RA	[1]		
RA	Kulper G.G., Enmark E., Gustafsson J.;		
RT	"ORPHAN RECEPTOR";		
RL	Patent number WO9709348-A/4, 13-MAR-1997.		
RL	KAROBIO AB (SE).		
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REFERENCE 1 (bases 1 to 1560)
AUTHORS Mosselman,S., Polman,J. and Dijkema,R.
TITLE ER beta: identification and characterization of a novel human
estrogen receptor
JOURNAL FEBS Lett. 392 (1), 49-53 (1996)
MEDLINE 96354875
REFERENCE 2 (bases 1 to 1560)
AUTHORS Mosselman,S.
JOURNAL Direct Submission
Submitted (04-JUL-1996) S. Mosselman, N.V. Organon, Biotechnology
and Biochemistry, PO box 20 Oss, Molenstraat 110 Oss, 5340 BH,
NETHERLANDS

FEATURES
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CDS
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BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;
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RESULT 8
LOCUS RNAJ2602 1650 bp DNA
DEFINITION Rattus norvegicus mRNA for estrogen receptor beta (clone pcDNA.ERbeta).

ACCESSION AJ002602
NID 93077648
KEYWORDS estrogen receptor beta.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1650)
Aldridge, T.C.
Tissue specific responses to estrogen: an explanation based on
differential activation of multiple estrogen receptors with
different estrogen response elements
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1650)
Aldridge, T.C.
JOURNAL Direct Submission
AUTHORS Submitted (17-Apr-1997) Aldridge T.C., Molecular Endocrinology
TITLE Group, ZENECA Central Toxicology Laboratory, Alderley Park,
Macclesfield, Cheshire SK10 4TU, ENGLAND
JOURNAL 3 (bases 1 to 1650)
Aldridge, T.C.
Direct Submission
AUTHORS Submitted (18-Nov-1997) Aldridge T.C., Molecular Endocrinology
TITLE Group, ZENECA Central Toxicology Laboratory, Alderley Park,
Macclesfield, Cheshire SK10 4TU, ENGLAND
JOURNAL revised by [3]
REMARK Location/Qualifiers
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DEFINITION	Rattus norvegicus estrogen receptor beta mRNA, complete cds.		
ACCESSION	U57439		
NID	91373280		
KEYWORDS	1		
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Mymorpha; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 8 to 2555)		
AUTHORS	Kulper,G.G., Enmark,E., Peltö-Huikko,M., Nilsson,S. and Gustafsson,J.A.		
	Cloning of a novel receptor expressed in rat prostate and ovary Proc. Natl. Acad. Sci. U.S.A. 93 (12), 5925-5930 (1996)		
JOURNAL			
TITLE			
MEDLINE	96234066		
REFERENCE	2 (bases 1 to 2555)		
AUTHORS	Enmark,E.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-MAY-1996) Eva L. Enmark, Center for Biotechnology, NOVUM, Karolinska, Institute, NOVUM, Huddinge, S-141 57, Sweden		
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AC	A61583:		
NI	e1262491		
DT	09-MAR-1998 (Rel. 54, Created)		
DT	09-MAR-1998 (Rel. 54, Last updated, Version 0)		
DE	Sequence 1 from Patent WO9709348.		
NW			
OS	Rattus rattus (black rat)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia;		
CC	Sciurognathi; Muridae; Murinae; Rattus.		
RN	[1]		
RA	Kulper G.G., Enmark E., Gustafsson J.;		
RT	"ORPHAN RECEPTOR";		
RL	Patent number WO9709348-A/1, 13-MAR-1997.		
RL	KAROBIO AB (SE).		
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LOCUS	15	1215 bp	mRNA	PRI	06-JUL-1998
DEFINITION	Homo sapiens estrogen receptor beta isoform 5/6 mRNA, partial cds.				
ACCESSION	AF074599				
NID	93289022				
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1215)				
TITLE	Bradenberger, A.W., Lebovic, D., Taylor, R.N. and Jaffe, R.B.				
JOURNAL	Homo sapiens estrogen receptor beta 5/6 splice variant, partial cds unpublished				
REFERENCE	2 (bases 1 to 1215)				
AUTHORS	Bradenberger, A.W., Lebovic, D., Taylor, R.N. and Jaffe, R.B.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-JUN-1998) Reproductive Endocrinology Center, University of California, San Francisco, 513 Parnassus, San Francisco, CA 94143-0556, USA				
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481	GCTCCCGAGAGAGATGTGGTACCGCCTTGTCCGAGACAGACAGAAATGCCCGAGAC	540			
746	gtctcccgagagagagatgtgtgtgtacgcgctgtgtcgagacagagaagTgcgcgagagc	805			
541	AGCTGACTGTGCCCGCAAGGCAAGAGAAATGGCGGCCACGCGCCGAGTGCGGAGC	600			
806	agctgactgtgtccgccaagagccaagaagaatgtgTgcgccaTgcgcccagTgcggagac	865			
601	TGCTGTGGACCCCTGAGACCCCGAGAGAGCTGTGCTCAACCTCTCGAGAGTGGACCGC	660			
866	tgtctgtcTgaagccctgagcccgagccagctgtgtctcaacctctgtgaggtctgacgcg	925			
926	cccatgtgtgtatcagccgcccacgtgtgccttaccagagccctccatgatgatgtccc	985			
721	TACCAAGTGTGGCCGACAAGAGTGTGTACATATATACGCTGGGCGAAGAGATTCCG	780			
986	tgaccaagTgtgcgacaagaagtgtgtatacatgatcagctTgcggccagaagaattccg	1045			

Db 781 G 781
Qy 1046 g 1046

Search completed: Tue Nov 3 04:15:08 1998
Job time : 2567 secs.

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W I S E R (TM)

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MPearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:51:42 1998; Maspar time 278.07 Seconds

Tabular output not generated. 824.913 Million cell updates/sec

Title: >US-08-906-365-1

Description: (1-1686) From US08906365.seq

Perfect Score: 1686

N.A. Sequence: 1 cagccattatctgcccac.....agaccacagctcagttga 1686

Comp: gtcggaatattgacgggtg.....tcttggtgtcagagtcac

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 188442 segs, 68026449 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.451; Variance 5.146; scale 1.837

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1667	98.9	1936	38	T88415	Human oestrogen recep	0.00e+00
2	1452	86.1	1460	29	T62843	Human oestrogen recep	0.00e+00
3	1434	85.1	1434	37	T88412	Human oestrogen recep	0.00e+00
4	1247	74.0	1251	37	T88413	Human oestrogen recep	0.00e+00
5	1247	74.0	1251	37	T88413	Human oestrogen recep	0.00e+00
6	1136	67.4	1256	38	T62842	Human oestrogen recep	0.00e+00
7	1010	59.9	1458	29	T62844	Rat oestrogen recep	0.00e+00
8	197	11.7	4963	17	T06873	Mouse oestrogen recep	0.00e+00
9	197	11.7	4963	17	T06873	Mouse oestrogen recep	0.00e+00
10	195	11.6	2092	2	N70880	PhCMV*-1 promoter and	3.54e-124
11	127	7.5	206	15	N85976	CDNA encoding human o	1.18e-122
12	71	4.2	3460	25	T42193	Human estrogen recept	1.80e-71
13	68	4.0	2153	2	N80922	Fragment of pig oestr	6.97e-31
						Sequence encoding hum	8.56e-29

14	63	3.7	6244	13	076269	PhCMV*-1-controlled p	2.42e-25
15	63	3.7	6244	17	T06872	PhCMV*-1 promoter and	2.42e-25
16	59	3.5	2992	20	T06491	Human heptoma retino	1.30e-22
17	59	3.5	2992	11	065572	Human liver hap CDNA.	1.30e-22
18	59	3.5	2992	13	079934	Human liver hap CDNA.	1.30e-22
19	58	3.4	1912	2	010388	Encodes skin-specific	6.17e-22
20	58	3.4	2334	38	V05701	Mutant nuclear glucoc	6.17e-22
21	58	3.4	2521	3	020542	Mouse retinoic acid r	6.17e-22
22	58	3.4	2740	3	020541	Mouse retinoic acid r	6.17e-22
23	58	3.4	5040	2	N80916	Sequence encoding the	6.17e-22
24	56	3.3	1913	18	T05202	Murine retinoic acid	1.38e-20
25	55	3.3	2989	1	N90093	Human Hap (hepatoma)	6.46e-20
26	55	3.3	6176	27	T49226	Plasmid pGR0403r for	1.38e-20
27	56	3.3	7257	31	T68656	Green fluorescent pro	1.38e-20
28	53	3.1	1231	6	037761	Sequence of a 1.23 kb	1.40e-18
29	53	3.1	1785	2	012005	Human TR2-9 DNA bindi	1.40e-18
30	53	3.1	2029	2	012004	Human TR2-5 androgen	1.40e-18
31	53	3.1	2221	2	012003	Human TR2-11 DNA bind	1.40e-18
32	53	3.1	2458	2	012006	Human TR2-7 DNA bind	1.40e-18
33	53	3.1	3014	33	T84747	Human progesterone re	1.40e-18
34	53	3.1	3014	35	T94756	Human progesterone re	1.40e-18
35	50	3.0	1351	13	079935	Human liver RAR-beta	1.35e-16
36	51	3.0	1576	2	010226	Clone pGEM-hRARgamma	2.96e-17
37	51	3.0	1903	2	010389	Encodes human Retinoi	2.96e-17
38	51	3.0	1903	18	T05196	Human retinoic acid r	2.96e-17
39	50	3.0	2249	2	N80921	Sequence encoding hum	1.35e-16
40	51	3.0	3569	29	T63407	Androgen receptor CDN	2.96e-17
41	51	3.0	3569	1	N91772	Human androgen recept	2.96e-17
42	51	3.0	3715	1	012001	Full-length human and	2.96e-17
43	49	2.9	204	1	N81164	Base substituted E.co	6.11e-16
44	44	2.9	3762	31	T73334	Human neuron-derived	6.11e-16
45	47	2.8	387	19	T09863	Modified human glucoc	1.23e-14

ALIGNMENTS

RESULT	1
ID	T88415 standard; CDNA; 1936 BP.
AC	T88415:
DT	20-APR-1998 (first entry)
DE	Human oestrogen receptor protein CDNA #2.
KW	Oestrogen receptor protein; steroid; alternative splicing; estradiol;
KW	estone; estril; screening; ss.
OS	Homo sapiens.
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	77..1669
FT	/*tag= a
FT	/product= oestrogen receptor
FT	EP-798378-A2.
PN	01-OCT-1997.
PD	25-MAR-1997; 200903.
PF	22-NOV-1996; EP-203284.
PR	26-MAR-1996; EP-200820.
PA	(ALKU) AKZO NOBEL NV.
PI	Dijkema R, Mosselman S;
DR	WPI: 97-473188/44.
DR	P-RSDB; W33215.
PT	DNA encoding estrogen receptor - useful in screening assay to
PT	Identify novel ligands or hormonal analogues
PS	Claim 5; Page 33-35; 45pp; English.
CC	This sequence encodes a novel estrogen binding protein isolated from
CC	human testis cDNA in order to study upstream translation-initiation
CC	codons using 5' RACE-PCR technology. This receptor is able to bind and
CC	be activated by estradiol, estone and estril, can be used in a screening
CC	assay for the identification of new drugs e.g. novel ligands or hormonal
CC	analogues.
SO	Sequence 1936 BP; 462 A; 514 C; 511 G; 449 T;
Query Match	98.9%; Score 1667; DB 38; Length 1936;
Best Local Similarity	99.9%; Pred. No. 0.00e+00;
Matches	1668; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	1 cagcaatcttggaacattatgacattgtgctctcttctgcaagtggtttctca 60

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|||||
QY 18 caccgaactcttggaacacttaataagacttctgctcctctctcgaagtgcttccaa 77
Db 61 gctttctctcaagaacatgatatataaaactccactcgaagcttaattctcctctc 120
QY 78 gctgtctactcaagaacatgatatataaaactccactcgaagcttaattctcctctc 137
Db 121 ctacaactgcatgaatccatcttaacccttgagacagcgctccatatacatctctc 180
QY 138 ctacaactgcatgaatccatcttaacccttgagacagcgctccatatacatctctc 197
Db 181 ctatgtagacagccaactgaatatccagcatgacatctatagcctctgtgtatga 240
QY 198 ctatgtagacagccaactgaatatccagcatgacatctatagcctctgtgtatga 257
Db 241 ttacagacatcccgcaactgcatgaatcttgaaagtgtggtcgtctgagacacaaag 300
QY 258 ttacagacatcccgcaactgcatgaatcttgaaagtgtggtcgtctgagacacaaag 317
Db 301 cccaatgtgtgtgagccaacacactgagacacttctcctcttaagtgtcactcgcagtt 360
QY 318 cccaatgtgtgtgagccaacacactgagacacttctcctcttaagtgtcactcgcagtt 377
Db 361 atcacatctgtatctgagaaactcaaaagagtcctctgtgtgtgaagcaagatcgctagaaca 420
QY 378 atcacatctgtatctgagaaactcaaaagagtcctctgtgtgtgaagcaagatcgctagaaca 437
Db 421 caccctactctttaaacagagagacactgaaagagaggttgatgagaaacgttgagcaag 480
QY 438 caccctactctttaaacagagagacactgaaagagaggttgatgagaaacgttgagcaag 497
Db 481 cccgtgtactgtgtccaaaggttcaaaagagagatgtcactctgtcgtctgtcgaagcattaa 540
QY 498 cccgtgtactgtgtccaaaggttcaaaagagagatgtcactctgtcgtctgtcgaagcattaa 557
Db 541 cgcactcgagatatcaactatgtgaagtcgtgtgtgtgaagagatgaagcctttttaaaag 600
QY 558 cgcactcgagatatcaactatgtgaagtcgtgtgtgtgaagagatgaagcctttttaaaag 617
Db 601 aagcactcaagagacataatgatatattgtgtccagctcaaaactcaagttacatcagataa 660
QY 618 aagcactcaagagacataatgatatattgtgtccagctcaaaactcaagttacatcagataa 677
Db 661 aaacccgagcgaagagctgtccagagccttcgcagacttcggaagtgttaacgaagtgtgaatgt 720
QY 678 aaacccgagcgaagagctgtccagagccttcgcagacttcggaagtgttaacgaagtgtgaatgt 737
Db 721 gaagtgtgtgtgtccgagagagagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
QY 738 gaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 797
Db 781 cgaagcagcagctgtgacactgtgcccgcgaagcgaagagagagagagagagagagagagagag 840
QY 798 cgaagcagcagctgtgacactgtgcccgcgaagcgaagagagagagagagagagagagagagag 857
Db 841 ggcggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
QY 858 ggcggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 917
Db 901 tgaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 960
QY 918 tgaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 977
Db 961 gatgtcccttgaccagaggtgtgcccgaagaagaggtgtgtacatgacagatgtgtgtgtgtgtgtgt 1020
QY 978 gatgtcccttgaccagaggtgtgcccgaagaagaggtgtgtacatgacagatgtgtgtgtgtgtgtgt 1037
Db 1021 gatcccgagcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
QY 1038 gatcccgagcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1097
Db 1081 gatgagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140

```

```

QY 1098 gatgagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1157
Db 1141 ctgtgtccagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
QY 1158 ctgtgtccagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1217
Db 1201 aatcttgaacatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
QY 1218 aatcttgaacatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1277
Db 1261 agaatatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
QY 1278 agaatatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1337
Db 1321 agcagccagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
QY 1338 agcagccagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1397
Db 1381 tgcttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
QY 1398 tgcttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1457
Db 1441 ggcctaactctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
QY 1458 ggcctaactctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1517
Db 1501 tctgtcacaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
QY 1518 tctgtcacaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1577
Db 1561 gaatgtccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620
QY 1578 gaatgtccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1637
Db 1621 agagagacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1669
QY 1638 agagagacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1686

```

RESULT
 2
 ID T62843 standard; cDNA: 1460 Bp.
 AC T62843;
 NC 08-JUN-1997 (first entry)
 DE Human oestrogen receptor beta (ER-beta) cDNA.
 KW Orphan receptor; oestrogen receptor beta; ER-beta;
 KW nuclear receptor; prostate cancer; benign prostatic hyperplasia;
 KW ovary cancer; cardiovascular disease; osteoporosis;
 KW environment; pollutant; ss.
 OS Homo sapiens.
 FH Key
 FT cds Location/Qualifiers
 FT 3..1460
 PN W09709348-A2.
 PD 13-MAR-1997.
 PE 09-SEP-1996; E03933.
 PR 08-SEP-1995; GB-018272.
 PR 15-MAR-1996; GB-005550.
 PR 11-APR-1996; GB-007532.
 PR 08-MAY-1996; GB-009576.
 PA (KARO-) KARO BIO AB.
 PI Enmark E, Gustafsson J, Kuiper GG;
 DR WPI: 97-192842/17.
 DR P-PSDB: W14724.
 PT New isolated oestrogen receptor beta - used to develop prods. for
 PT treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
 PT disease
 PS Claim 6, Fig 13B, 45pp. English.
 CC A cDNA clone (T62843) codes for a novel human oestrogen receptor-
 CC related nuclear receptor (W13724), designated ER-beta. It was
 CC isolated from a human testis cDNA library using rat ER-beta cDNA
 CC (see also T62842) as probe. The human ER-beta gene was mapped
 CC to chromosome 14 region 14q22-23. Rat, human and mouse ER-beta
 CC (W14723-25) can be used to isolate molecules for use in the

[illegible][illegible]

QY	793	agctgcgcgaacgagcgtctgcacatctgtcccgagcaagggccaaagaaagtgtgcggccacgcgcgcc	852
Db	1048	cgggaggaagggcgactacgtctgtagacacctgtgaccccaagaagaactgtgtctcaacccctctg	1107
QY	853	cgagtcgcgagggctgcgtcgtctgtgaacggcccttgagcccccgagcagctagctgtccacccctctg	912
Db	1108	gaagcttgaaaccaaccaatgtctgtgtgagccgctccaccagctacgtcccttcacacgaagcctcc	1167
QY	913	gaggtctgagccggccccaatgtgtctgatcagccgcgccaaagtgcgcctctcaacgagcctcc	972
Db	1168	atgtatgatgtctccctcactaagctgtgcggaacaagaaactgtgcacatgtatgtctgtggcc	1227
QY	973	atgagatgtctcccttgaccacaagattgtgcgcgaacaagagattgtgtacacatagtacagctgtgccc	1033
Db	1228	aagaaatcccccttgctctttgttggaactgaagcctcttttgacaacaagtccggctcttaagaagc	1287
QY	1033	aagaaagatccccggctctctgtgtggaactcagaccgtgtctccgaacaagtggtggtctcttgagaagc	1097
Db	1288	tgctgtgatagagtggtctaaatgtgtgtggaactgattgtgcgtccacatctgcacaccccggaag	1347
QY	1093	tgttgatgagaggtgtgttaatgatgtgaggtgcgtgatgtgtggtgcctcaatttgacaccccggaag	1155
Db	1348	ctcaatttcgctcccgaccctcgattctgtgacagagatgtagaagtggaagtgcgtlaagaagagatt	1407
QY	1153	ctcatcttgtctccacagatctgttctctgtgacaagagatgaaaggtgaatactgtaagaagatt	1212
Db	1408	cttggaaatcttttgacagctccctctgtgcgagacgactcaagtgctccggtgtagtataaactccag	1467
QY	1213	cttggaaactcttttgacagctccctctgtgcgacactactcaagaagtcttgaaagttaaaactccaa	1272
Db	1468	cacaaagagatactccctctgtgtgaagggcatgatctctccataaccacagatgtgacacctgtg	1527
QY	1273	cacaaagatatctctctgtgtlcaagggccatgatctctgatactccagatatgtacacctctg	1333
Db	1528	gcttctgcgaaaccagagggcgcaagaagtacgggaagcttgacacacctactgtgaacgcggctg	1587
QY	1333	gtccacagcgaccaccagagatgtctgtacagacgacgggaagctgtgctcatctgtgtgaacgcgctg	1392
Db	1588	acagatgcccccggtcgtctgtgtgtgattgtgcgaagaagtgtgtatctctctccagacgaactgaatc	1647
QY	1393	accgatactgttctgtgtgtgtgtgtatgtgcgaagaagcgatctctctccacagacgaactacatg	1453
Db	1648	cgactgagccaactccctcgatagctctctctcttcacgctacgtaacgatacgaataaaggcgatg	1707
QY	1453	cgctctgtgctaaacctcccgatgctctctgtctccacgctcaaggaatgvcgagtaacaagggcgag	1512
Db	1708	gaacatctgtctcagcagcatgaaagtgcgaaaaatgtgtctccggtgtgatgaacctgtctgtcgag	1767
QY	1513	gaacatctgtctcacaacatgaaagtgcgaaaaatgtgtctccagtgatgaacctgtctgtcgag	1572
Db	1768	atgtctgaatgtctcaacgcgcttcgagggctacaagcttcctcaatctcgggtgtctagtgtcgagc	1827
QY	1573	atgtctgaatgtcccccagctgtctctcggtgtgcgaatctctccatccacacggtgtctcgagtcgagc	1633
Db	1828	tcaacagagagcagtaagaacaagaagagctcccaacaactacagcttaagta 1881	
QY	1653	ccggcagagagcagtaaaagaacaagaaggtcctccgaacccaacagatctcaagta 1686	
RESULT			
ID	7	T62844 standard; cDNA: 1458 BP.	
AC	T62844;		
DE	08-JUN-1997 (first entry)		
KM	Mouse oestrogen receptor beta (ER-beta) cDNA.		
KW	Orphan receptor; oestrogen receptor beta; ER-beta; nuclear receptor; prostate cancer; benign prostatic hyperplasia; ovary cancer; cardiovascular disease; osteoporosis; environment; pollutant; SS.		
OS	Mus sp.		
PN	W09709348-A2.		
PD	13-MAR-1997.		
PF	09-SEP-1996; E03933.		

PR	08-SEP-1996; GB-018272.
PR	15-MAR-1996; GB-005550.
PR	11-APR-1996; GB-007532.
PR	08-MAY-1996; GB-009576.
PA	(KARO-) KARO BIO AB.
P1	Enmark E, Gustafsson J, Kuiper GG;
DR	WPI; 97-192842/17.
DR	P-PDB; M14725.
PT	New isolated oestrogen receptor beta - used to develop prods. for
PT	treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
PT	disease
PS	Claim 6, Fig 14B, 45P; English.
CC	A cDNA clone (T62844) codes for a novel mouse oestrogen receptor-
CC	related nuclear receptor (M13725), designated ER-beta. Rat, human
CC	and mouse ER-beta (M14723-25) can be used to isolate molecules for
CC	use in the treatment of cardiovascular diseases, central nervous
CC	system diseases, osteoporosis, prostate or ovarian cancer or benign
CC	prostatic hyperplasia and to test environmental chemicals for
CC	oestrogenic activity.
SQ	Sequence 1458 BP; 365 A; 373 C; 403 G; 317 T;
Query Match	59.9%; Score 1010; DB 29; Length 1458;
Best Local Similarity	84.6%; Pred. No. 0.00e+00;
Matches 1234; Conservative	0; Mismatches 224; Indels 0; Gaps 0;
Db	1 atggatcttaagcgcgtgtagtgaactaaagtgtcccaacagaccggyaaccty 60
QY	229 atggaactttataagccctgcgtgtgatattacaacatccacgaatgttactaatcttg 288
Db	61 gaaggctggccgttcgccagacttgcagccaagtgcatagtgcataacctctggacac 120
QY	289 gaaagtggtccgtgcgycagacaccaagaagcccaatgtgtgtgccaaccctggcgac 348
Db	121 cctctcccttagccaccacatgcctctctctaigtacagacctcaaaaagt 180
QY	349 ctctcccttagtgtcatcgcgcagatcatcacatctgtatgtaggaacctcaaagagt 408
Db	181 ccttggtgtgaagcaagttcatactagaacaacctgtgcgtgaacagaagacccttaag 240
QY	409 cccttggtgtgaagcaagctcgtgaacaacaccttaccttgaacagaagacacttgaaa 468
Db	241 aaggaagcttggggagcgcgtgtgtgcagccctgttaactagttcaagcaccagaagagat 300
QY	469 aggaaggttatgtggaaacgctgtgcgcagcccttactgtgtccaggttcaaaagagat 528
Db	301 gtccactctctgcccgtctcagtatataatgcactgtggttcaatlcaggtygtctgcc 360
QY	529 gctcaactctgcgtctgtctgcagcattagcctcgcgagatatcaactatgagtctgtcg 588
Db	361 tttgaagatgttaaagcctttttaaaagaagcatccaagacataatgactatctgt 420
QY	589 tgtgaagatgttaaagcctttttaaaagaagcatccaagacataatgactatctgt 648
Db	421 ccagccagagatcaatfagacatagaacaagccgggttaaaactccagcgccttcgca 480
QY	649 ccagctacaaatcagtttacatcgaataaaaaaccggcgcaagagctgcaggccttcgca 708
Db	481 ctctcgaagtglttaagaaagtgaatgtgtcaagtgctgatatccagagagaagaagtgtg 540
QY	709 cttcggaagtglttaagaaagtgtgaatgtgtgaagtgtgctcccggaagaagagatgtgg 768
Db	541 tacgcaatagtaagacaagaagagaagtgcagcgagcaagtgcatctcctgacaagcc 600
QY	769 tacccctctgtgcggagacagagaagtgcgcagacagcagctgtgcgcggaagcc 828
Db	601 aaggaataaccagttggccacacccccgggtgaaggaagctactgcctgaaactcttgagccc 660
QY	829 aaggaataatgvcggccacacgcccccgagttggggagctgtgcctgcggagcccttgaagccc 888
Db	661 gagcagctggtgtctaacctctgtgaagctatgcacccaatgtgtcagttgagctgtcc 720
QY	889 gagcagctagtgctaacctctctgtgaagctatgcagccccaatgtgtcagttcagcagccccc 948

QY 545 tctgcagcgattacgcacgcgggatatcactatggagctctgctgtgtgaaggatgtaagg 604
Db 2425 tctctttaaaaggcaatggaaggcaagcacaataattatgtctgtgaagaatgact 2484
||| ||||| | | | | | | | | | | | | | | | |
QY 605 cctttttaaaagagcatcacaagacataatgattatatltgtccagctacaacacagt 664
Db 2485 gcaattgtataaataccgcaggaaaaaactgccgcgcgtgtgccttaagaagtgtctgc 2544
| | | | | | | | | | | | | | | | | | | | | |
QY 665 gtacaatcgataaaaccggcgcaagagctgccagcgctgcgacttcggaagtgttacg 724
Db 2545 aagctggcatggt 2557
||| ||| |||||
QY 725 aagtggaatcgt 737

Search completed: Tue Nov 3 04:56:31 1998
Job time : 289 secs.

W I S E N H (TM)

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MSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:27:57 1998; MasPar time 27.56 Seconds

Tabular output not generated. 702,514 Million cell updates/sec

Title: >US-08-906-365-2

Description: (1-530) from US08906365.pep

Perfect Score: 3904

Sequence: 1 MDIKNSPSSINSPPSYNCSQ.....ECSPAEDSKSEGSQNPQSQ 530

Scoring table: PAM 150

Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: plr56

1:plr1 2:plr2 3:plr3 4:plr4 5:nr13d

Statistics: Mean 48.751; Variance 99.595; scale 0.489

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3532	90.5	477	2	S71400 estrogen receptor bet	0.00e+00
2	1735	44.4	586	1	ORXLE estrogen receptor - A	0.00e+00
3	1710	43.8	589	1	ORCHE estrogen receptor - C	0.00e+00
4	1683	43.1	595	1	ORHUE estrogen receptor 1 -	0.00e+00
5	1669	42.8	599	1	ORHSE estrogen receptor - m	0.00e+00
6	1663	42.6	600	1	ORRTE estrogen receptor - r	0.00e+00
7	1654	42.4	595	2	I47140 estradiol receptor -	5.58e-103
8	1516	38.8	574	2	A37197 estrogen receptor - r	1.66e-274
9	1503	38.5	535	2	S58224 oestrogen receptor -	7.90e-272
10	1473	37.7	701	2	S64737 80K estrogen receptor	1.19e-265
11	807	20.7	433	2	B29345 steroid hormone recep	4.93e-130
12	799	20.5	433	2	S58087 estrogen receptor rel	1.97e-128
13	800	20.5	521	2	A29345 steroid hormone recep	1.24e-128
14	681	17.4	923	2	A39596 progesterone receptor	6.28e-105
15	671	17.2	923	2	I53280 progesterone receptor	5.99e-103
16	666	17.1	933	1	ORHUP progesterone receptor	5.84e-102
17	662	17.0	930	2	A25923 progesterone receptor	3.61e-101
18	614	15.7	742	1	ORHUGA glucocorticoid recept	1.04e-91
19	614	15.7	777	1	ORHUGA glucocorticoid recept	1.04e-91
20	608	15.6	776	1	S44047 glucocorticoid recept	1.57e-80
21	597	15.3	786	2	A35466 progesterone receptor	2.25e-88
22	594	15.2	771	2	A54273 glucocorticoid recept	8.72e-88
23	586	15.0	783	1	A25691 glucocorticoid recept	3.21e-86

24	579	14.8	133	2	S26595 estrogen receptor - b	7.52e-85
25	577	14.8	795	1	ORRTG glucocorticoid recept	1.85e-84
26	571	14.6	899	2	A35895 androgen receptor - m	2.75e-83
27	570	14.6	902	2	B40494 androgen receptor - r	4.31e-83
28	567	14.5	919	2	A39248 androgen receptor - h	1.66e-82
29	564	14.4	910	2	A34721 androgen receptor A -	6.39e-82
30	562	14.4	981	2	A41401 mineralocorticoid rec	1.57e-81
31	557	14.3	74	5	IHCQA humanCHICKEN ESTROGEN	1.48e-80
32	557	14.3	74	5	IHCQE humanCHICKEN ESTROGEN	1.48e-80
33	557	14.3	75	5	IHCPE humanCHICKEN ESTROGEN	1.48e-80
34	560	14.3	911	2	B34721 androgen receptor B -	3.82e-81
35	547	14.0	71	5	IHCQB humanCHICKEN ESTROGEN	1.31e-78
36	543	13.9	758	2	S60586 androgen receptor - c	7.84e-78
37	544	13.9	758	2	S60586 glucocorticoid recept	5.01e-78
38	533	13.7	533	2	S37781 retinoid x receptor b	6.86e-76
39	529	13.6	410	2	S26669 retinoic acid recepto	4.10e-75
40	529	13.6	448	2	A34418 H-2 region II binding	4.10e-75
41	529	13.6	448	2	D41727 retinoid x receptor b	4.10e-75
42	529	13.6	451	2	A41651 retinoic acid recepto	4.10e-75
43	523	13.4	984	2	A29513 mineralocorticoid rec	5.96e-74
44	514	13.2	467	2	S26668 retinoic acid recepto	3.29e-72
45	514	13.2	467	2	A47278 retinoid x receptor a	3.29e-72

ALIGNMENTS

RESULT 1
ENTRY 1 S71400 #type complete
TITLE estrogen receptor beta - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 26-Feb-1998

ACCESSIONS S71400
REFERENCE S71400
#authors Mosselman, S.; Polman, J.; Dijkema, R.
#journal FEBS Lett. (1996) 392:49-53
#title ER-beta: identification and characterization of a novel human estrogen receptor.

#accession S71400

#molecule_type mRNA

#residues 1-477 #label MOS

#cross-references EMBL:X99101

CLASSIFICATION #superfamily estrogen receptor; erba transforming protein homology

KEYWORDS DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor; transcription regulation; zinc finger

FEATURE

94-355 #domain erba transforming protein homology #label ERBA\

96-116 #region zinc finger CCCC motif\

132-156 #region zinc finger CCCC motif\

167-182 #region nuclear location signal\

52 #binding_site phosphate (Ser) (covalent) (by MAP kinase) #status predicted

96,99,113,116 #binding_site zinc (Cys) #status predicted

132,138,148,151 #binding_site zinc (Cys) #status predicted

SUMMARY #length 477 #molecular_weight 53363 #checksum 8603

Query Match 90.5%; Score 3532; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	1	MWSTPSVNTNLEGGPGQTSSPNVLPTRPGHLSLVYHROLSHYAEPQKSPWCEASL	60
OY	54	MWSTPSVNTNLEGGPGQTSSPNVLPTRPGHLSLVYHROLSHYAEPQKSPWCEASL	113
DB	61	EHLLPVNRETLKRRKSGNRCASPVTPGSKRDARHCACVDSAGYHGWSCCEGKAFF	120
OY	114	EHLLPVNRETLKRRKSGNRCASPVTPGSKRDARHCACVDSAGYHGWSCCEGKAFF	173
DB	121	KRSIGGHNDYICPATNOCTIDKNRRKSCQACRLRCYEGWYKCGSRRRCRGYRLVRQR	180
OY	174	KRSIGGHNDYICPATNOCTIDKNRRKSCQACRLRCYEGWYKCGSRRRCRGYRLVRQR	233

Db	181	SASOLHOCAGAKKSGGAPRVRELLIDALSPEDVYTLLEADPHYLISRPAPTEAS	240
Qy	234	SADBDLHOCAGAKKSGGAPRVRELLIDALSPEDVYTLLEADPHYLISRPAPTEAS	293
Db	241	MMMSLTKLADKELYHMISMAKKIFGEVBLSLFDVRLLESCWMEVLMGMJMSIDHPGK	300
Qy	294	MMMSLTKLADKELYHMISMAKKIFGEVBLSLFDVRLLESCWMEVLMGMJMSIDHPGK	353
Db	301	LIFAPDVLDRDEGCVEGILIEFDMLLATSRRELKQHKEXYLCVKAMILLNSSMYPL	360
Qy	354	LIFAPDVLDRDEGCVEGILIEFDMLLATSRRELKQHKEXYLCVKAMILLNSSMYPL	413
Db	361	VTATODADSSKRLAHNLNAVYDALVWYIAKSGISSQOOSMRALMLMLLSHYVHSAKGM	420
Qy	414	VTATODADSSKRLAHNLNAVYDALVWYIAKSGISSQOOSMRALMLMLLSHYVHSAKGM	473
Db	421	EHLNMKCKNNVPYVDLLEMLNHAHVJGCKSSITGSECSFPAEDSKSKESQNPQSQ	477
Qy	474	EHLNMKCKNNVPYVDLLEMLNHAHVJGCKSSITGSECSFPAEDSKSKESQNPQSQ	530

RESULT	2
ENTRY	
TITLE	ORXLE #type complete
ORGANISM	estrogen receptor - African clawed frog
DATE	#formal name Xenopus laevis #common name African clawed frog
	28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 15-Jun-1996
ACCESSIONS	A40807
REFERENCE	A40907
#authors	Weiler, I.J.; Lew, D.; Shapiro, D.J.
#journal	Mol. Endocrinol. (1987) 1:355-362
#title	The Xenopus laevis estrogen receptor: sequence homology with

#cross-references MUID:903319277

```
##molecule_type mrna
##residues 1-586 ##label WEI
##cross-references GB:P20735
```

COMMENT The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize specific DNA sequences upstream of transcriptional start sites.

CLASSIFICATION #superfamily estrogen receptor; erba transforming protein

KEYWORDS DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor; transcription regulation; zinc finger

FEATURE	
1-174	#domain amino-terminal #label NH2\
175-266	#domain DNA binding #status predicted #label DNA\
178-448	#domain erba transforming protein homology #label ERBA\
178-201	#region zinc finger CCCC motif\
214-237	#region zinc finger CCCC motif\
251-266	#region nuclear location signal\
229-544	#domain steroid binding #status predicted #label STR\
180,183,197,200	#binding_site zinc (Cys) #status predicted
216,222,232,235	#binding_site zinc (Cys) #status predicted
231	#binding_site phosphate (Ser) (covalent) #status predicted

```
SUMMARY
#length 586 #molecular-weight 66080 #checksum 9991
```

Query Match	44.48;	Score 1735;	DB 1;	Length 586;
Best Local Similarity	50.88;	Pred. No. 0.00e+00;		
Matches 247;	Conservative 112;	Mismatches 107;	Indels 20;	Gaps 16

Db 70 YSSSLSYAASSETFG-SSSLTGHT-LNNVPPSPVFLAKLPOLSPFIHHGQQVYYL 127
|:::|::: ::|::| |::: ::||::|::|

QY	43	YPAWTF--YSPAVNMYSPISVNTJNEGPRQOTSPNVMTPEHLSPLYVNR--OLSHLYA	100
Db	128	ESBEGTF-AVREAAPEFFYRSSDNRRSGREHMSANDKGPMSMESTKREYCAVCSDY	186
QY	101	EPQSPWCEASLEHILPVNRETLKRVSG--NR-CASPVTGP-G--SKRAHFCAYCSDY	155
Db	187	ASGHYGVWSCGEGCKAFKFKRSIOGHNDYMCPATNOCTIDKNRRKSCOACRLKCYEYGM	246
QY	156	ASGHYGVWSECGCKAFKFKRSIOGHNDYICPATNOCTIDKNRRKSCOACRLKCYEYGMV	215
Db	247	KGGIRKDRGGRLLKHKROKEDEOKDNDVDSBELRTSINWPNDSYKMKRISPLYSLAEQ	306
QY	216	KCGSRRECGRILRV--RQSRADQLH-CAGKAKRSG--HAPRYRLILDA-LS--PEQ	267
Db	307	LISALMEAAPIYVSEHDSFKPLSEASAMTLLTNIADRELVHIMINAKRVYGFVDLTJLHD	366
QY	268	LVLTLLEAPHPHVISRPSA-PFEASIMMSLTKLADRELVHIMISYMKKIPGEVELSLFD	326
Db	367	QVHLLECAMLEILWGLIWRSVHEPGLSPFAPNLLDRNOCRCVEGLVEIPLMTYATR	426
QY	327	QVRLLSECMVMVLMMGLMWRSIDHPGLIIPAPDVLDRDESKCYEGLLEIFDMILATTS	386
Db	427	FRMRRLGEEFICLSIILLNSGYUTFLSSTLESIEDTDLHILDKIIDPLVYHFMKSG	486
QY	387	FRELTKQIKETLCYKAMILLNMSMYPLVTANQDADSSKRLAHU-LNVVDALVWVIKSG	445
Db	487	LSLOOQORRLAOLLILSHIRHMSNKGMEHLISYKCKKNVPLVDLLLEMDAHHIRPKD	546
QY	446	ISSQOOSMRLANLMLTSHVHNASNKGMEHLINMKCKNVVYDLLLEMANAHVLRCKS	505
Db	547	KTTTQE 552	
QY	506	SITGSE 511	

RESULT	3	QRCHE	#type complete
ENTRY		estrogen receptor - chicken	
TITLE		#formal_name Gallus gallus	#common_name chicken
ORGANISM		06-Mar-1992	#sequence_revision 14-Jul-1994
DATE		06-Mar-1992	#text_change

Accessions 03-Sep-1997
 Reference A40914; S07192
 A40914
 #authors Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schul
 Greene, G.L.; O'Malley, B.W.
 #journal Mol. Endocrinol. (1987) 1:25-35
 #title Structural organization and regulation of the chicken
 estrogen receptor.
 #cross-references M01D:85318621

```

#status      not compared with conceptual translation
#molecule_type  mRNA
#residues    1-589  #label MAX

```

REFERENCE
#authors Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.;
 Bornert, J.M.; Chambon, P.
#journal EMBO J. (1986) 5:891-897
#title The chicken oestrogen receptor sequence: homology with *v-erbA*
 and the human oestrogen and glucocorticoid receptors.
#cross-references MJD:86247578

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#accession      S07192
#status         preliminary
#molecule_type mRNA
#residues       1-256, 'E', 258-589 ##label KRU
#cross-references EMBL:X03805; NID:g63378; PID:g63380

```

COMMENT The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.

CLASSIFICATION #superfamily estrogen receptor; erba transforming protein
 KEYWORDS DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor; transcription regulation; zinc finger

FEATURE
 1-173 #domain amino-terminal #label NH2
 174-255 #domain DNA binding #status predicted #label DNA
 177-450 #domain erba transforming protein homology #label ERBA
 213-235 #region zinc finger CCCC motif
 230-265 #region nuclear location signal
 294-566 #domain steroid binding #status predicted #label STB
 179,182,196,199 #binding-site zinc (Cys) #status predicted
 215,221,231,234 #binding-site zinc (Cys) #status predicted
 230,299 #binding-site phosphate (Ser) (covalent) #status predicted

SUMMARY #length 589 #molecular-weight 66773 #checksum 793

Query Match 43.8%; Score 1710; DB 1; Length 589;
 Best Local Similarity 51.6%; Pred. No. 0.00e+00;
 Matches 247; Conservative 112; Mismatches 99; Indels 21; Gaps 14;

DB 69 YGSLTSLVPTSESEF-SSSLAGFHS-LNNVPPSVYFIQTAPQLSPFIHHSGQVPIYL 126
 43 YPAMTF-YSPAVMNYSPISPVNTLEGGPGROTTSPNVLPTEHLSPLVYHR-QLCHLYA 100
 127 ENEGSGFGRAPAPAFYRPPSSDNRHSIRERSSSTNEKSGSLMSTKTRCAVANDYA 186
 101 EPQKSPWCARSLEHTL-PVNETTLKRVSGNFCASPVTP-G-SKRDHFCVAVSDYA 156
 187 SCYHGVMSCEGCKAFKFKSIQNDYMCPTNOCTIDKNRRKSCQACRLKCYEVMK 246
 157 SCYHGVMSCEGCKAFKFKSIQNDYICPATNOCTIDKNRRKSCQACRLKCYEVMK 216
 247 GGIKRDRCGRMKQRQREEDDSNGEASSTELRAPLMTSPVLYVKNKNSPALSLTA 306
 217 CSRRRCRCYLRVRRORSADEQLHCAGKAKRSQGHAPRV-R-E-LTL-----D--ALS--P 265
 307 EOMVSLLEAPPIYSEVDPNRPNENASMTLLTNLADRELHVMNNAKRVGFDLTL 366
 266 EDVLTLLEAPPPHVLIS-RPSAPFTEASMMSLTKLAKRELHVMNNAKRVGFELEL 324
 367 HDQVHLECAMLEIIMIGLVMSMEHPKGLFAPNLLDRNKGCEVGEVIEFDMLATA 426
 325 PQVRLCESCMVEVLNMGMLWRSIDHPKGLIFAPDLVDREKCYEGILEIFDMLATT 384
 427 AFRPMNLGEEFVCIKSIILNSGYTFLSTLSLEERDYIHRVLDKITDTLILHMAK 486
 385 SFRREIKLOHKEVLCYKAMILLNSSMYPLVTATQDADSSRLAH-LNNAVTDALVAVIAK 443
 487 SGLSLQOQRRLAOLLIIISHIRHMSNGMEHLNKKCNVAVLYLLEMDAHLHA 545
 444 SGISSQOQMRLANLMLLSHVHRAHNAKMEHLNKKCNVAVLYLLEMDAHLHA 502

RESULT 4
 ENTRY ORHUE #type complete
 TITLE estrogen receptor 1 - human
 ALTERNATE_NAMES ER1; estrogen receptor alpha
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 28-May-1986 #sequence_revision 28-May-1986 #text_change 20-Mar-1998
 ACCESSIONS A94284; A93376; A43021; S27143; S34000; A41925; B41925;
 A03244; C41925; D41925
 REFERENCE A94284
 #authors Greene, G.L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Y.;
 #journal Science (1986) 231:1150-1154
 #title Sequence and expression of human estrogen receptor
 #cross-references MUID:86122927
 #accession A94284

#molecule-type mRNA
 #residues 1-595 #label GR1
 #cross-references GB:M12674; NID:g182192; PID:g182193
 REFERENCE A93376
 #authors Green, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.;
 #journal Nature (1986) 320:134-139
 #title Human estrogen receptor cDNA: sequence, expression and homology to v-erb-A.
 #cross-references MUID:86146892
 #accession A93376
 #molecule-type mRNA
 #residues 1-595 #label GR2
 #cross-references GB:X03635; NID:g31233; PID:g31234
 REFERENCE A43021
 #authors Ponglikitmongkol, M.; Green, S.; Chambon, P.
 #journal EMBO J. (1988) 7:3385-3388
 #title Genomic organization of the human oestrogen receptor gene.
 #accession A43021
 #molecule-type DNA
 #residues 143-161;205-225;244-264;356-374,'G',376;402-442;447-460,
 'P',462-467;508-528 #label PON
 #cross-references EMBL:X62462; NID:g31201; PID:g31205
 REFERENCE S27140
 #authors Keaveney, M.; Klug, J.; Gannon, F.
 #journal DNA Seq. (1992) 2:347-358
 #title Sequence analysis of the 5' flanking region of the human estrogen receptor gene.
 #accession S27143
 #status preliminary; translation not shown
 #molecule-type DNA
 #residues 1-115 #label KEA
 #cross-references EMBL:X62462; NID:g31201; PID:g31205
 REFERENCE S34000
 #authors Pfeiffer, U.; Pecarotta, F.; Castagnetta, L.; Vidali, G.
 #journal Cancer Res. (1993) 53:741-743
 #title Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive human breast cancer cell lines.
 #accession S34000
 #status preliminary
 #molecule-type mRNA
 #residues 216-254,367-399,'G',401-434 #label PFE
 #cross-references EMBL:X73067; NID:g579865; PID:g939886
 #title Characterization of estrogen receptor variant mRNAs from the authors translated the codon GGC for residue 400 as Val
 REFERENCE A41925
 #authors Dotzlaw, H.; Alkhalaf, M.; Murphy, L.C.
 #journal Mol. Endocrinol. (1992) 6:773-785
 #title Characterization of estrogen receptor variant mRNAs from human breast cancers.
 #cross-references MUID:92293154
 #accession A41925
 #molecule-type mRNA
 #residues 1-214,'ELPTLC' #label DOT
 #cross-references GB:M69297; NID:g182218; PID:g182219
 #experimental_source clone 4; breast cancer
 #note sequence has been revised after extraction from NCBI backbone
 #note the complete sequence of neither the nucleotide nor the protein is shown in this paper
 #accession B41925
 #status significant sequence differences
 #molecule-type mRNA
 #cross-references GB:M69296
 #experimental_source clone 24; breast cancer
 #note sequence extracted from NCBI backbone (MGBIN:106597)
 #comment The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. In the absence of 19and, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of

COMMENT The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular

#journal	Nucleic Acids Res. (1987) 15:2499-2513
#title	Molecular cloning and characterization of rat estrogen

Accession	Source	Organism	Gene	Protein	Length	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score
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[illegible]

Matches	140;	Conservative	84;	Mismatches	108;	Indels	22;	Gaps	14
Db	101	RCLVCGDIASGHHYGYASCEACAFKRTIQGNIETSCPATNECEITTKRRKSCQACRF	160						
Qy	147	HFCVACSDYASGYHYGWSCEGCAKFFKRSIOGHNDYICPATNCTIDKNNRKSQCARTL	206						
Db	161	MKCLAKVMTKEGVLDVY--R-GGRQRY-KRRIDSENSPLSIDISPAKKPLTKIYS--	214						
Qy	207	RKCEYGVAMKCGSRRKRCGRFLVYRQRQSADEQLHCAGKARSGGHARVVELLDALSPE	266						
Db	215	YL-L-VAEPDKLYAM-PPDDVPEGDIALTTLCIDLADEIVFLTSMKAKH1PGFENLTIGD	271						
Qy	267	QLVLTLEAEPPHYLIRSPAPFLTEASMMMSLTFLADKELVHMTSMWAKK1PGFVELSLFD	326						
Db	272	QMSLLQASMMETILIGIVYRSLPYDRLKAYAEYIDMEHSRLV-GLLELYRALLQVLR	330						
Qy	327	QVRLESCMWEVLMMGLMMRSIDHPGKILFAPDLVLRDGGKCEVGEILEIFDMLATTSR	386						
Db	331	YKRLAKKEEPPVMTKALALANSDMY--T---ENLEAVQKLDLLH--BALQ-DYLS-	380						
Qy	387	FRELKLOHKEVLCYKAMILLNS-SMYPDYATQADSSRKALHNLNAVTDALVWVIKSG	445						
Db	381	-QRHEEPRRAGKILVTPLRQTLAQAIVOHFYSVYKLOGKPMHLEFMELEAKV	433						
Qy	446	ISSQOQSRMLANLMLLSHYRHASNKGMHLLCNKNVYVYDLDLEMLAHV	499						
RESULT	12								
ENTRY		S58087	#type complete						
TITLE			estrogen receptor related protein - mouse						
ORGANISM			#format_name Mus musculus #common_name house mouse						
DATE			13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 31-Oct-1997						
ACCESSIONS		S58087							
REFERENCE		S58087							
#authors		Petersson, K.; Svensson, K.; Mattsson, R.; Carlsson, B.; Ohlsson, R.; Berkenstam, A.							
#submission		submitted to the EMBL Data Library, July 1995							
#description		Expression of a novel member of estrogen response element-binding nuclear receptors is restricted to the early stages of chorion formation during mouse embryogenesis.							
#accession		S58087							
#status		preliminary							
#molecule_type		mRNA							
#residues		1-433	#label PET						
#cross-references		EMBL:X89594							
CLASSIFICATION		#superfamily unassigned erba-related proteins; erba transforming protein homology steroid hormone receptor; zinc finger							
KEYWORDS									
FEATURE									
101-352									
SUMMARY		#domain erba transforming protein homology #label ERBA #length 433 #molecular_weight 44400 #checksum 1075							
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Best Local Similarity		38.7%; Pred. No. 1.97e-128;							
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Db	101	RCLVCGDIASGHHYGYASCEACAFKRTIQGNIETSCPATNECEITTKRRKSCQACRF	160						
Qy	147	HFCVACSDYASGYHYGWSCEGCAKFFKRSIOGHNDYICPATNCTIDKNNRKSQCARTL	206						
Db	161	MKCLAKVMTKEGVLDVY--R-GGRQRY-KRRIDSENSPLSIDISPAKKPLTKIYS-N	215						
Qy	207	RKCEYGVAMKCGSRRKRCGRFLVYRQRQSADEQLHCAGKARSGGHARVVELLDALSPE	266						
Db	216	-L-LGV-EODKLYAM-PPNDIPGEDIALTTLCIDLADEIVFLTSMKAKH1PGFENLTIGD	271						
Qy	267	QLVLTLEAEPPHYLIRSPAPFLTEASMMMSLTFLADKELVHMTSMWAKK1PGFVELSLFD	326						
Db	272	QMSLLQASMMETILIGIVYRSLPYDRLKAYAEYIDMEHSRLV-GLDDYRALLQVLR	330						
Qy	327	QVRLESCMWEVLMMGLMMRSIDHPGKILFAPDLVLRDGGKCEVGEILEIFDMLATTSR	386						
Db	331	YKRLAKKEEPPVMTKALALANSDMY--T---ENLEAVQKLDLLH--BALQ-DYLS-	380						
Qy	387	FRELKLOHKEVLCYKAMILLNS-SMYPDYATQADSSRKALHNLNAVTDALVWVIKSG	445						
Db	381	-QRHEEPRRAGKILVTPLRQTLAQAIVOHFYSVYKLOGKPMHLEFMELEAKV	433						
Qy	446	ISSQOQSRMLANLMLLSHYRHASNKGMHLLCNKNVYVYDLDLEMLAHV	499						

Db	331	YKLLVEKEEFILKATALANSQSW--I---ENLEAYOKLDLH---EALQ-DVETS	380
Oy	387	FRELLOHREYLCVRAAILNS-SMPLVYATADADSSKRLAHLLNVYDALVWYIAKSG	445
Db	381	-ORHEEPRRAGKLLMTLPLLRQTAARAVOHFYSVKLOGKVRMKLEPLEMEAAV	433
Oy	446	ISSQOOSMRLANLMLLSHVRRASNKGMHEILLNMCKKNVFPVYDLLEMANHY	499
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TITLE		steroid hormone receptor ERRI precursor - human	
ALTERNATE_NAMES		estrogen-related receptor	
ORGANISM		#formal.name Homo sapiens	#common.name man
DATE		15-Dec-1988	#sequence_revision 15-Dec-1988
		12-Sep-1997	#text_change
ACCESSIONS		A29345; A49074	
REFERENCE		A29345	
#authors		Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.	
#journal		Nature (1988) 331:91-94	
#title		Identification of a new class of steroid hormone receptors.	
#cross-references		EMBL:88122546	
#accession		A29345	
#molecule_type		mRNA	
#residues		1-521	#label GIG
#cross-references		EMBL:X51416; NID:g36608; PID:g36609; EMBL.Y00290	
REFERENCE		A49074	
#authors		Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.	
#journal		Genes Dev. (1993) 7:2206-2219	
#title		Sv40 early-to-late switch involves titration of cellular transcriptional repressors.	
#accession		A49074	
#status		preliminary	
#molecule_type		protein	
#residues		166-169, 'X', 171-173	#label WIL
CLASSIFICATION		#superfamily unassigned	estrogen-related proteins; estrogen-related protein
KEYWORDS		DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger	
FEATURE			
174-434		#domain	estrogen transforming protein homology
176-196		#region	zinc finger
212-236		#region	zinc finger
SUMMARY		#length 521	#molecular_weight 55742
			#checksum 5840
Query Match		20.5%;	Score 800; DB 2; Length 521;
Best Local Similarity		39.98;	Pred. No. 1.24e-128;
Matches 141; Conservative		74;	Mismatches 128; Indels 10; Gaps 7;
Db	174	RCLTCGVDAVSQYHYVAVACACAFKFRKTQSGIESCPASNECETTKRRKACQACRF	233
Oy	147	HFCAVCSQDPAASGTHYVMSCEGKAFKFSIGDNHYICATQCTIDKRRKSCQACRL	206
Db	234	TKCLRVGMLKEGVRLDVRVGRGKVRKRPEDVLPFRPG-P-PRAGPLAVAGGPKTAAPV	291
Oy	207	RKCEYGVGKSCSRRCRC-GYRLVRQRQSDQLHCAQAKRSGGNAPRVRELLDRLSP	265
Db	292	NALVGHLLVPERBEKLYAMPDPAGDPDGHLPVALVLCDFPRLVYVTTISMASIGFSSLSL	351
Oy	266	EDLVLTLEAEPRPHV-L-ISRPSAPFTASMSMSLTKLADKELVHMTSMARKIGFEVELSL	324
Db	352	SDQMSVGLQVMEVAVLQVQORSLPQDELAFADVLYLD-EEGARAAGLGEALALQVL	410
Oy	325	PDQVALLBESQWMEVLLMGLMRSIDIRPKLITFRPDLVLDDEBKCVGSLIFIDMLATT	384
Db	411	RRLQALRLEREYVLLKALALANSDSVNIHDEDRILMSCEKLLH--EAL--LEYAGRA	465
Oy	385	SFFRELKDHKEKLYCAKAILLNSMYPLVATQADSSKRLAHLLNVAIDALVWYIAKS	444
Db	466	GGGGAERRRAGRLTLTLPLRLQTAQVLAHFGVALLGKVRPNHKLFLVLEIA	518

RESULT	ENTRY	14	
445	GISSQOOSMRLANLMLSHVRASNKGEHLLNKKCKNVVPYDULLEMLNA	497	
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	ORGANISM	progestrone receptor B form - mouse	
	DATE	#formal_name Mus musculus #common_name house mouse	
		20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change	
		31-Oct-1997	
	ACCESSIONS	A39596	
	REFERENCE	A39596	
	#authors	Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.	
	#journal	Biochemistry (1991) 30:7014-7020	
	#title	Molecular cloning, sequence analyses, and expression of	
		complementary DNA encoding murine progesterone receptor.	
	#cross-references	MOID:9129/759	
	#accession	A39596	
	#status	preliminary	
	##molecule_type	mRNA	
	##residues	1-923 ##label SCH	
	##cross-references	GB:M68915; GB:J05333; NID:g200471; PID:g200472	
	CLASSIFICATION	#superfamily progesterone receptor; ezba transforming protein	
		homology	
	KEYWORDS	DNA binding; nucleus; steroid hormone receptor; transcription	
		regulation; zinc finger	
	FEATURE		
	555-819	#domain ezba transforming protein homology #label ERBA\	
	557-577	#region zinc finger	
	593-617	#region zinc finger	
	SUMMARY	#length 923 #molecular-weight 99073 #checksum 6627	
	Query Match	17.4%; Score 681; DB 2; Length 923;	
	Best Local Similarity	30.88; Prid. No. 6,28e-105;	
	Matches	123; Conservative 112; Mismatches 138; Indels 27; Gaps 27;	
Db	491 AAPGTAAAPATYOPLG-LINGLPOLG-Y-QAAVLKDSLPQVVPYLYLRPDSASQSPQY	547	
Qy	81 PTPGHSPLVYVHOLSHLVAEPKSWCABRLDLEPTL-VNRETLK-RKVGNCACAPVT	138	
Db	548 GFDSLPQ-KICLICGDEASCHGYVLTGSCGVFFKRAMEGOHNYLCAGRDCIYDKIR	606	
Qy	139 GPGSKRDHAFCAVCSYASGYHGVSCGCAKFFKRSIQGHNDYICPATNQCITDKNR	198	
Db	607 KNCACACLRCCACAGVLT-GGRFK-KFNKAVKATLDGVALPQSGVLPNSQALSQRT	664	
Qy	199 KSCACACLRCCVGVGWKCGSRERCGYLTVRRSSADE-QL-HCAGKAKRSGGHAPVR	256	
Db	665 FSPNOETOLVP-ELINLMSIEPDVYYAGHDNTRKPDTSLSLTGNOGEOQLSVYKMS	723	
Qy	257 -ELLIDA-LSPEDVLVLTLEAPPHYLISRPSA-PPTESAMMSLTAKADELVHMTSWA	313	
Db	724 KSLPGFNLHIDQITLQYSWMSLWFLGSRKYSKHVSGQMLYFAPDLILN-EQ-R-MK	780	
Qy	314 KRIGFVELSLFDQVRLSCSWEVYLMGLMRSIDH-PGKIL-FAPDLVLDREGRKVE	371	
Db	781 E-LSFYSCLTMMQIQOEYKQLQVHEEFLCKAVLLILNT-1-PLGGRSQSGFEENRKS	837	
Qy	372 GLEIEIFDM-L-L-ATTSRFRELKQHEKELCYKAMILLNMSMYPLVATODADSSRLAH	428	
Db	838 YIRELIKALIG-LRQKGVPTSQRFQYLTLLDLSLDLYKQ	876	
Qy	429 LLNAVTDALVYIAKSGISSQOOSMRLANL-MLLSHYRH	467	
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	ORGANISM	progesterone receptor - rat	
	DATE	#formal_name Rattus norvegicus #common_name Norway rat	
		02-Apr-1996 #sequence_revision 02-Aug-1996 #text_change	
		25-Apr-1997	
	ACCESSIONS	I53280; B23733; A23733	
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		Park-Sarge, O.R.; Mayo, K.E.	

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DB 140 RETLKRKLSGSSCASPVYTPSPNAKRAHFCAVCSDYASGYHYGWPCEGCAFFKRSIOGH 199
QY 121 RETLKRKVSNGNRCAAPVYTPGSKRAHFCVCDYASGYHYGWPCEGCAFFKRSIOGH 180
DB 200 NDYICPATNOCTIDKRRKRSQACRLKCYEVGMVKGSRRERCGYRIVRRORSSEQYH 259
QY 181 NYICPATNOCTIDKRRKRSQACRLKCYEVGMVKGSRRERCGYRIVRRORSSEQYH 240
DB 260 CLSKARRNGHAPRVKRELLDLSPEQVLTLEAEPPNVLVSRPMPFEASMMMSLTK 319
QY 241 CAGKARRSGHAPRVKRELLDLSPEQVLTLEAEPPNVLVSRPMPFEASMMMSLTK 300
DB 320 LADKELVHMISWAKKIPGFVELSLDQVRLLESCMVEYLMGMRSIDHFGKLIFFAPDL 379
QY 301 LADKELVHMISWAKKIPGFVELSLDQVRLLESCMVEYLMGMRSIDHFGKLIFFAPDL 360
DB 380 VLDROGKCVESGILEIFDMILATTSRFRKLQHKREYLCYKAMILLNSSMYPLVATODA 439
QY 361 VLDROGKCVESGILEIFDMILATTSRFRKLQHKREYLCYKAMILLNSSMYPLVATODA 420
DB 440 ESSRKLTHLNAVYDALVWYIAKSGISSQOOSMRILNMLLSHVHSHKGMHEHTLSMK 499
QY 421 DSRKLAHLNAVYDALVWYIAKSGISSQOOSMRILNMLLSHVHSHKGMHEHTLSMK 480
DB 500 CKNVVYVDLLEMLNAHLRGYKPSISGSECSSTEDSKNKESSONLQSO 549
QY 481 CKNVVYVDLLEMLNAHLRGYKPSISGSECSSTEDSKNKESSONLQSO 530

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RESULT 2
ID Q92731 PRELIMINARY: PRT: 477 AA.
AC Q92731
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ESTROGEN RECEPTOR BETA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-TESTIS.
RA MOSELMAN S., POLMAN J., DIKEMA R.;
RA FEBS LETT. 392:49-53(1996).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DB EMBL: X99101; E255390; -.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR. 1.
DR PFAM: PF00104; hormone_rec.
DR RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW ZINC-FINGER.
SQ SEQUENCE 477 AA: 5383 MW; 4E76E987 CRC32;

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Query Match 90.5%; Score 3532; DB 4; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNYSIPSNVNTLEGGRGRTTSPNVLMPTPGHLSPLVYHROLSHYAEPOKSPWCARSLE 60
QY 54 MNYSIPSNVNTLEGGRGRTTSPNVLMPTPGHLSPLVYHROLSHYAEPOKSPWCARSLE 113
DB 61 EHTLPNRETLLKRVSGNRCASPVYTPGSKRAHFCVCDYASGYHYGWPCEGCAFF 120
QY 114 EHTLPNRETLLKRVSGNRCASPVYTPGSKRAHFCVCDYASGYHYGWPCEGCAFF 173
DB 121 KKSIOGHNDYICPATNOCTIDKRRKRSQACRLKCYEVGMVKGSRRERCGYRIVRROR 180
QY 174 KKSIOGHNDYICPATNOCTIDKRRKRSQACRLKCYEVGMVKGSRRERCGYRIVRROR 233
DB 181 SADEOLHCAGKARRSGHAPRVKRELLDLSPEQVLTLEAEPPNVLVSRPMPFEAS 240

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QY 234 SADEOLHCAGKARRSGHAPRVKRELLDLSPEQVLTLEAEPPNVLVSRPMPFEAS 293
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QY 294 MMSLTKLADKELVHMISWAKKIPGFVELSLDQVRLLESCMVEYLMGMRSIDHFGK 353
DB 301 LIFAPDLVLDROGKCVESGILEIFDMILATTSRFRKLQHKREYLCYKAMILLNSSMYPL 360
QY 354 LIFAPDLVLDROGKCVESGILEIFDMILATTSRFRKLQHKREYLCYKAMILLNSSMYPL 413
DB 361 VYATODADSSRKLHLNAVYDALVWYIAKSGISSQOOSMRILNMLLSHVHSHKGM 420
QY 414 VYATODADSSRKLHLNAVYDALVWYIAKSGISSQOOSMRILNMLLSHVHSHKGM 473
DB 421 EHLNKKCKNVVYVDLLEMLNAHLRGYKPSISGSECSSTEDSKNKESSONLQSO 477
QY 474 EHLNKKCKNVVYVDLLEMLNAHLRGYKPSISGSECSSTEDSKNKESSONLQSO 530

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RESULT 3
ID O60685 PRELIMINARY: PRT: 513 AA.
AC O60685
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ESTROGEN RECEPTOR BETA 3 ISOFORM.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA MOORE J.T., MCKEE D.D., SLENTZ-KESLER K., MOORE L.B., JONES S.A.,
RA SU J.L., HORNE E.L., KLEWER S.A., LEHMAN J.M., WILLSON T.M.;
RA SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DB EMBL: AF060555; G3091286; -.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR. 1.
DR RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW ZINC-FINGER.
SQ SEQUENCE 513 AA: 57518 MW; 1CC02BEC CRC32;

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Query Match 89.1%; Score 3480; DB 4; Length 513;
 Best Local Similarity 97.7%; Pred. No. 0.00e+00;
 Matches 470; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

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DB 1 MDIKRSPSSLNSSSYNCSQSLPLEHGSITYPSSYVSHHEYPAMTYSPAVNNYSIPS 60
QY 1 MDIKRSPSSLNSSSYNCSQSLPLEHGSITYPSSYVSHHEYPAMTYSPAVNNYSIPS 60
DB 61 NTYNLEGGRGRTTSPNVLMPTPGHLSPLVYHROLSHYAEPOKSPWCARSLEHTLPVN 120
QY 121 RETLKRKVSNGNRCAAPVYTPGSKRAHFCVCDYASGYHYGWPCEGCAFFKRSIOGH 180
DB 181 NDYICPATNOCTIDKRRKRSQACRLKCYEVGMVKGSRRERCGYRIVRRORSSEQYH 240
QY 181 NDYICPATNOCTIDKRRKRSQACRLKCYEVGMVKGSRRERCGYRIVRRORSSEQYH 240
DB 241 CAGKARRSGHAPRVKRELLDLSPEQVLTLEAEPPNVLVSRPMPFEASMMMSLTK 300
QY 241 CAGKARRSGHAPRVKRELLDLSPEQVLTLEAEPPNVLVSRPMPFEASMMMSLTK 300
DB 301 LADKELVHMISWAKKIPGFVELSLDQVRLLESCMVEYLMGMRSIDHFGKLIFFAPDL 360
QY 301 LADKELVHMISWAKKIPGFVELSLDQVRLLESCMVEYLMGMRSIDHFGKLIFFAPDL 360
DB 361 VLDROGKCVESGILEIFDMILATTSRFRKLQHKREYLCYKAMILLNSSMYPLVATODA 420
QY 361 VLDROGKCVESGILEIFDMILATTSRFRKLQHKREYLCYKAMILLNSSMYPLVATODA 420

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Db 421 DSSRLAHLNVTDALVWYIAKSGISSQOOSRLANLMLSHVHAKSLISMLFNL 480
 QY 421 DSSRLAHLNVTDALVWYIAKSGISSQOOSRLANLMLSHVHAKSLISMLFNL 479
 Db 481 R 481
 QY 480 K 480

RESULT 4
 ID 060608 PRELIMINARY: PRT: 495 AA.
 AC 060608:
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR BETA2 SPLICED VARIANT.
 OS HOMO SAPIENS (HUMAN)
 OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA MOORE J.T., MCKEE D.D., MOORE L.B., JONES S.A., SU J.-L., HORNE E.L.,
 KLIMMER S.A., LEHMANN J.M., WILSON T.M.;
 SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 EMBL; AF051428; G2961559;
 DR PROSITE: PS00031: NUCLEAR RECEPTOR: 1.
 KW RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 ZINC-FINGER.
 SQ SEQUENCE 495 AA; 55483 MW; 4461D854 CRC32;

Query Match 89.0%; Score 3476; DB 4; Length 495;
 Best Local Similarity 98.5%; Pred. No. 0.00e+00;
 Matches 470; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Db 1 MDKNSPSSLSNPSSYSCOSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMNTSIPS 60
 QY 1 MDKNSPSSLSNPSSYSCOSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMNTSIPS 60
 Db 61 NVTNLEGGGRTQTPNVIMPTPGHLSPLVHRQSLHLYAEPOKSPWCARSLEHTLPVN 120
 QY 61 NVTNLEGGGRTQTPNVIMPTPGHLSPLVHRQSLHLYAEPOKSPWCARSLEHTLPVN 120
 Db 121 RETLKRKVSNGRCASPYTGPGSRDHAFCAYCSDYASGYHYGWSCEGCKAFPKRSIQGH 180
 QY 121 RETLKRKVSNGRCASPYTGPGSRDHAFCAYCSDYASGYHYGWSCEGCKAFPKRSIQGH 180
 Db 181 NDYICPATNOCTIDKNRRKSCQACRLRKYEVGMVKGSRRECGRYLVKRSADBDLH 240
 QY 181 NDYICPATNOCTIDKNRRKSCQACRLRKYEVGMVKGSRRECGRYLVKRSADBDLH 240
 Db 241 CAGKAKRSNGHAPRVRELLDALSPDLVLTLLAEPPHYLISRPAPFTASMMSLRK 300
 QY 241 CAGKAKRSNGHAPRVRELLDALSPDLVLTLLAEPPHYLISRPAPFTASMMSLRK 300
 Db 301 LADKELVHISNAKKIPGFEVLSLFDQVRLLESCEMVEVLMGMLMRSIDHPGLIAPDL 360
 QY 301 LADKELVHISNAKKIPGFEVLSLFDQVRLLESCEMVEVLMGMLMRSIDHPGLIAPDL 360
 Db 361 VLDRDEGKCEVGLIEIFDMILATTSFRRELKLOHKEYLCVAKMILNNSNYPLVATODA 420
 QY 361 VLDRDEGKCEVGLIEIFDMILATTSFRRELKLOHKEYLCVAKMILNNSNYPLVATODA 420
 Db 421 DSSRLAHLNVTDALVWYIAKSGISSQOOSRLANLMLSHVHAKSLISMLFNL 477
 QY 421 DSSRLAHLNVTDALVWYIAKSGISSQOOSRLANLMLSHVHAKSLISMLFNL 476

RESULT 5
 ID 008537 PRELIMINARY: PRT: 485 AA.
 AC 008537;

DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR BETA.
 GN ESTRB.
 OS MUS MUSCULUS (MOUSE)
 OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=OVARY;
 RA TREMBLAY G.B., TREMBLAY A., COPELAND N.G., GILBERT D.J., JENKINS N.A.,
 LABRIE F., GIGUERE V.;
 RL NATURE 11:353-365(1997).
 -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U081451; G1912468; -.
 DR MGD; MG1:109392; ESTRB.
 DR PROSITE: PS00031: NUCLEAR RECEPTOR: 1.
 DR PFAM; PF00104; hormone_rec.
 DR RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 ZINC-FINGER.
 SQ SEQUENCE 485 AA; 54058 MW; B6BF7C7 CRC32;

Query Match 84.0%; Score 3278; DB 11; Length 485;
 Best Local Similarity 88.9%; Pred. No. 0.00e+00;
 Matches 431; Conservative 34; Mismatches 20; Indels 0; Gaps 0;

Db 1 MTFYSPAVMNTSIPSSTGMLEGGPVROTASPNVIMPTGSHLSPLATHCSSLIYAEPOKS 60
 QY 46 MTFYSPAVMNTSIPSSTGMLEGGPVROTASPNVIMPTGSHLSPLATHCSSLIYAEPOKS 105
 Db 61 PWCARSLEHTLPVNRETLKRKVSNGRCASPYTGPGSRDHAFCAYCSDYASGYHYGWS 120
 QY 106 PWCARSLEHTLPVNRETLKRKVSNGRCASPYTGPGSRDHAFCAYCSDYASGYHYGWS 165
 Db 121 CEGCKAFPKRSIQGHNDYICPATNOCTIDKNRRKSCQACRLRKYEVGMVKGSRRECG 180
 QY 166 CEGCKAFPKRSIQGHNDYICPATNOCTIDKNRRKSCQACRLRKYEVGMVKGSRRECG 225
 Db 181 YRIVRQRSASEOVHCLNKAARTSGHTPVKELLNLSPEOLVLTLLAEPPHYLSRP 240
 QY 226 YRIVRQRSASEOVHCLNKAARTSGHTPVKELLNLSPEOLVLTLLAEPPHYLSRP 285
 Db 241 SMPFTASMMSLTKLADKELVHISNAKKIPGFEVLSLFDQVRLLESCEMVEVLMGML 300
 QY 286 SMPFTASMMSLTKLADKELVHISNAKKIPGFEVLSLFDQVRLLESCEMVEVLMGML 345
 Db 301 RSLDHPGLIAPDLVLDRDEGKCEVGLIEIFDMILATTSFRRELKLOHKEYLCVAKMIL 360
 QY 346 RSLDHPGLIAPDLVLDRDEGKCEVGLIEIFDMILATTSFRRELKLOHKEYLCVAKMIL 405
 Db 361 LNSMYPPLATASQAEBSRLKTHLNAVTDALVWYIAKSGISSQOOSRLANLMLSHV 420
 QY 406 LNSMYPPLATASQAEBSRLKTHLNAVTDALVWYIAKSGISSQOOSRLANLMLSHV 465
 Db 421 RHLSKNGMHLNMAKKNVPPYDILLEMLNAHTLNGYSSISGSCCCTEDSKSREGSQ 480
 QY 466 RHLSKNGMHLNMAKKNVPPYDILLEMLNAHTLNGYSSISGSCCCTEDSKSREGSQ 525
 Db 481 NLOSQ 485
 QY 526 NPOSQ 530

RESULT 6
 ID 062986 PRELIMINARY: PRT: 485 AA.
 AC 062986:
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR BETA.
 OS RATUS NORVEGICUS (RAT).

[illegible]

Query Match	83.2%	Score 3250	DB 11	Length 485
Best Local Similarity	88.0%	Pred. No. 0.00e+00		
Matches 427	Conservative	36	Mismatches 22	Indels 0
				Gaps 0
Db	1	MAFSPAYMANYSVSSPTGNEGGPVROTASPNVLMPPISGHLSPLATHCGSSLLYAEPOKS	60	
Qy	46	MTFTSPAYMANYSISNTVNTNLEGGRGRTTSPNVLMPFPHLSPLVYHROLSHLAEPOKS	105	
Db	61	PMCEARSLEHTLPVNRRETLRKRLKLGSCASCPVTSPTKRDPAHFCAMVCSDAASYGHWMS	120	
Qy	106	PMCEARSLEHTLPVNRRETLRKRYVSGNRCASPVYGGPSGRDAHFCAMVCSDAASYGHWMS	165	
Db	121	CEGKAPFKRSIQGHNDYICPATNOCTIIDKNRKNCOACRLKCYEYGVYKCSGRRECG	180	
Qy	166	CEGKAPFKRSIQGHNDYICPATNOCTIIDKNRKNRSCACRLKCYEYGVYKCSGRRECG	225	
Db	181	YRVRROMSAEYHCVLKNKAKRTSGHPRYKELLNSLSPQOLVTLLEAPPVLYSRP	240	
Qy	226	YRVRROMSAEYHCVLKNKAKRTSGHPRYKELLNSLSPQOLVTLLEAPPVLYSRP	285	
Db	241	SMPTFASMMMSLTKLADKELVHIGAKKPIGFVELSLDQVYLLSCMMVEYLVAM	300	
Qy	286	SAPFTFASMMMSLTKLADKELVHIGAKKPIGFVELSLDQVYLLSCMMVEYLVAM	345	
Db	301	RSIDHPGKLIFAPDLVLDREGEKVEGILETFDMLATATARFRELKLOHKEYLCVKAMIL	360	
Qy	346	RSIDHPGKLIFAPDLVLDREGEKVEGILETFDMLATATSRFRELKLOHKEYLCVKAMIL	405	
Db	361	LNSSTYHLATASQAEBSRKLTHLINAVTDALVWIVKSRSSQOQSVRLANLMLLSHV	420	
Qy	406	LNSSTYHLATASQAEBSRKLTHLINAVTDALVWIVKSGISSQOQSMRLANLMLLSHV	465	
Db	421	RHISNKGHEHLSMKCKNVVPVYDLLLEMLNAHTLRGYSISGSGCSTEDSKSKSGSQ	480	
Qy	466	RHISNKGHEHLSMKCKNVVPVYDLLLEMLNAHVLRCCKSSITGSECSPADDSKSKSGSQ	525	
Db	481	NLQSQ 485		
Qy	526	NPQSQ 530		
RESULT	8	PRELIMINARY;	PRT;	503 AA.
ID	035785	AC	035785	
DT	01-JAN-1998	(TREMBL.REL. 05, CREATED)		
DT	01-JAN-1998	(TREMBL.REL. 05, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998	(TREMBL.REL. 06, LAST ANNOTATION UPDATE)		
DE	OESTROGEN RECEPTOR BETA2.			
GN	ERBETA.			
OS	RATTUS NORVEGICUS (RAT).			
CC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHIERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-WISTAR; TISSUE--PROSTATE;			
RA	ALDRIDGE T.C.;			
RL	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-SPRAGUE-DAWLEY;			
RA	PETERSEN D.N., TKALCEVIC G.T., KOZA-TAYLOR P.H., TURI T.G.,			
RL	BROWN T.A.;			
RL	ENDOCRINOLOGY 0:0-0(1998).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	EMBL; AJ002603; E1184907; -.			


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QY 106 PWCANSLHLEHLPVNRKTLKRVSGNRCASPVTPGSKRDHFCACVSDYASGYHGWMS 165
DB 121 CEGCKAFKRSIQG-----SRRRCG 141
QY 166 CEGCKAFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGMVCKGSRRCRG 225
DB 142 YRIVRORSSSEOVHCISKAKRNGGAPRVKELLSTLSPQVLVTLLEAPPVLSRP 201
QY 226 YRIVRORSSADEQLHCAGKAKRSGGHPRVRELLDLALSPQVLVTLLEAPPVLSRP 285
DB 202 SMPTEASMMSLTKLADKELVHMIGNAKPIGFVELSLDDQVLLSCMVEVLMGLMW 261
QY 286 SAPTEASMMSLTKLADKELVHMISNAKPIGFVELSLDDQVLLSCMVEVLMGLMW 345
DB 262 RSIDHPGKLIFFADVLDRDEGKCEGILEIFDMLATTSFRRLKQHKEXYLCVKAMIL 321
QY 346 RSIDHPGKLIFFADVLDRDEGKCEGILEIFDMLATTSFRRLKQHKEXYLCVKAMIL 405
DB 322 LNSMYPVLATADSSRKLAHLNAVTDALVWVIKSGISSQOQSMRLANLMLLSHV 381
QY 406 LNSMYPVLATADSSRKLAHLNAVTDALVWVIKSGISSQOQSMRLANLMLLSHV 465
DB 382 RHISNKGMEHLISMCKKNVVPYDILLEMNAHTLRGYKSSISGESSSTEDSKNKSQ 441
QY 466 RHISNKGMEHLISMCKKNVVPYDILLEMNAHTLRGYKSSISGESSSTEDSKNKSQ 525
DB 442 NLOSO 446
QY 526 NPOSO 530

RESULT 11
ID 055016 PRELIMINARY; PRT; 464 AA.
AC 055016;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ESTROGEN RECEPTOR BETA2 DELTA3.
GN ERBETA.
OS RATRUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RA [1]
RC SEQUENCE FROM N.A.
RA STRAIN-SPRAUE-DAMLEY;
RA PETERSEN D.N., TKALCEVIC G.T., KOZA-TAYLOR P.H., TURI T.G.,
RA BROWN T.A.;
RL ENDOCRINOLOGY 0:0-0(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF042061; G2801697;
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW ZINC-FINGER.
SQ SEQUENCE 464 AA; 51715 MW; 70679086 CRC32;

Query Match 60.1%; Score 2347; DB 11; Length 464;
Best Local Similarity 78.1%; Pred. No. 0.00e+00;
Matches 393; Conservative 34; Mismatches 19; Indels 57; Gaps 2;

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QY 226 YRIVRORSSADEQLHCAGKAKRSGGHPRVRELLDLALSPQVLVTLLEAPPVLSRP 285
DB 202 SMPTEASMMSLTKLADKELVHMIGNAKPIGFVELSLDDQVLLSCMVEVLMGLMW 261
QY 286 SAPTEASMMSLTKLADKELVHMISNAKPIGFVELSLDDQVLLSCMVEVLMGLMW 345
DB 262 RSIDHPGKLIFFADVLDRDEGKCEGILEIFDMLATTSFRRLKQHKEXYLCVKAMIL 321
QY 346 RSIDHPGKLIFFADVLDRDEGKCEGILEIFDMLATTSFRRLKQHKEXYLCVKAMIL 381
DB 382 RHISNKGMEHLISMCKKNVVPYDILLEMNAHTLRGYKSSISGESSSTEDSKNKSQ 441
QY 448 SQOQSMRLANLMLLSHVHISNKGMEHLISMCKKNVVPYDILLEMNAHTLRGYKSSIS 507
DB 442 SGSECSSTEDSKNKSQ 464
QY 508 TGSECSSTEDSKNKSQ 530

RESULT 12
ID 013012 PRELIMINARY; PRT; 573 AA.
AC 013012;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ESTROGEN RECEPTOR.
OS ANGILOLLA JAPONICA (JAPANESE EEL).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC EUTEICHTHYES; ACTINOPTERYGII; ANGILOLLIFORMES.
RA [1]
RC SEQUENCE FROM N.A.
RA TISSUE-LIVER;
RA TISSUE-LIVER;
RA TODO T.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA TODO T., ADACHI S., YAMAUCHI K.;
RL MOL. CELL. ENDOCRINOLOGY 119:37-45(1996).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AB003356; D1020638;
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR PFAM: PF00104; hormone-rec.
DR RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW ZINC-FINGER.
SQ SEQUENCE 573 AA; 63420 MW; A0B07849 CRC32;

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Query Match 57.4%; Score 2240; DB 13; Length 573;
Best Local Similarity 58.9%; Pred. No. 0.00e+00;
Matches 310; Conservative 101; Mismatches 98; Indels 17; Gaps 13;

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Db 270 RTORRGEGVNTQTOAOSASLTPEDLIRITIEAPEPEIYLMKELKPPTEDSMMSLTNL 329
 QY 244 KAKRGG-GHAPRREGLLDALSPLEQVLTLLEAEPPHV-LISRPSPAPTEASMMSLTKL 301
 Db 330 ADKELVNIISNAKKIPGVEVDLSDQVHLLCEGTEVLMIGMRSVDPHGKLTSPDLK 389
 QY 302 ADKELVNIISNAKKIPGVEVDLSDQVHLLCEGTEVLMIGMRSVDPHGKLTSPDLK 361
 Db 390 LNRDEGSCVEGILETFDMLVLAATSRFREKLQREYVCLAKIILNPNLCITSSSENREL 449
 QY 362 LDRDEGKCEGILETFDMLVLAATSRFREKLQREYVCLAKIILNPNLCITSSSENREL 420
 Db 450 ESRKKLMLDSVDALVWTAKKGLTQOOSARLAHLMLIAITRLHSNKGHELSNKK 509
 QY 421 DSSRLAHLMLAVDALVWTAKKGLTQOOSARLAHLMLIAITRLHSNKGHELSNKK 480
 Db 510 RKNVPLVDLLEMDANTMHSSRSASYSOSPSPMSQAOSOPP 555
 QY 481 CKNVVPYDILLEMLNAHVLKCKSSIT-GSECP-AEDSKSEGS 524

RESULT 13
 ID 091250 PRELIMINARY: PRT: 587 AA.
 AC 091250.
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR.
 OS POSPHILIA GUTTATA (ZEBRA FINCH).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC PASSERIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOTHALAMUS-PREOPTIC AREA;
 RA JACOBS E.C., ARNOLD A.P., CAMAGNONI A.T.;
 RL J. STEROID BIOCHEM. MOL. BIOL. 59:0-0(0).
 RL -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: L79911; G1449146; -.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR PFAM: PF00104; hormone_rec.
 DR PFM: PF00105; zfc-C4.
 KW RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 KW ZINC-FINGER.
 SQ SEQUENCE 587 AA; 66553 MW; 71DF4848 CRC32;

Query Match 43.6%; Score 1701; DB 13; Length 587;
 Best Local Similarity 51.6%; Pred. No. 0.00e+00;
 Matches 247; Conservative 112; Mismatches 99; Indels 21; Gaps 13;

Db 67 YSSTLLSYAPTSSEFG-SSSLAGFHS-LNSVSPVVFLOTAPHMSPFIIHHSQGVPTYL 124
 QY 43 YPAMTF-YSPAVMNTSISNTNTEGGRGROTPSPVPTGHLSPVLVHR-QLSHLTA 100
 Db 125 ENDGSGFGRAPAFYRPNSDNRHSIRERMSANKEGSLSMSESTRETRYCAVCNDYA 184
 QY 101 EPOKSPMCSEASLEHTL-PVNRRETLKRVYSGNRCASPYTGP-G-SKDAHRCVACSDYA 156
 Db 185 SGYHGVWSCGCGKAFRRSTOGHNDYMCPTNOCTIDKNRKSQAQRLKRCIYGVMMK 244
 QY 157 SGYHGVWSCGCGKAFRRSTOGHNDYMCPTNOCTIDKNRKSQAQRLKRCIYGVMMK 216
 Db 245 GGIKDRGRGVYMKOKROVERODSRNGEASSTELRAPTLMAISPLVKNKKRSPALSLTA 304
 QY 217 CGSRREKRGYLVRRQRSADEDLHCAGKAKKSGGHAIFYRE-LLL-----D-ALS--P 265
 Db 305 EOMVSALEAEPPVLYSEYDPPNRPNEASMMTLTNLADRELVHMINNAKRVGFDVTL 364
 QY 266 EQLVTLLEAEPPVLYS-REPAPTEASMMSLTKLADKELVNIISNAKKIPGVEVDL 324
 Db 365 HDQVHLLCEGTEVLMIGLWRSMEHPGKLFAPVLLDDRNGKCEGVEGVEITFDMLATA 424
 QY 325 FDOVALLCESCMEVLMIGLWRSMEHPGKLFAPVLLDDRNGKCEGVEGVEITFDMLATA 384

Db 425 AFRFMMNQGEEFVCKSLIILNSGVTFSLSTLSEEDKYIHRVLDKTIIDTLIIMAK 484
 QY 385 SFRRELKQHEKYEIVCKAMILNNSMYPVLTATODADSSRLAH-LTNVADALVWTAK 443
 Db 485 SGLSQOCHRRLAQOLLLSHRIHRSNKGHELYNMCKKNVPLVDLLEMLDAHRLA 543
 QY 444 SGISQOOSMRLANMLLSHVRAHSNKGHELYNMCKKNVPLVDLLEMLNAHVLNG 502

RESULT 14
 ID 013511 PRELIMINARY: PRT: 701 AA.
 AC 013511.
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE 80 KDA ESTROGEN RECEPTOR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BREAST.
 RX MEDLINE; 96174665.
 RA PINK J.J., WO S.Q., WOLF D.M., BILLIMORIA M.M., JORDAN V.C.;
 RL NUCLEIC ACIDS RES. 24:962-969(1996).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: U47678; G1197855; -.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR PFAM: PF00104; hormone_rec.
 DR PFM: PF00105; zfc-C4.
 KW RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 KW ZINC-FINGER.
 SQ SEQUENCE 701 AA; 78430 MW; 9A80F802 CRC32;

Query Match 37.7%; Score 1473; DB 4; Length 701;
 Best Local Similarity 56.9%; Pred. No. 0.00e+00;
 Matches 197; Conservative 85; Mismatches 49; Indels 15; Gaps 11;

Db 178 SAKERRYAVANDYASGYHYGVWSECGKAFRRSTOGHNDYMCPTNOCTIDKNRKS 237
 QY 142 SKRDHFCVAGSDYASGYHYGVWSECGKAFRRSTOGHNDYMCPTNOCTIDKNRKS 201
 Db 238 QACRLKRCIYGVMMKGIKRDGRGRLMKHRRDDEGREGVSGADMRANLMPSPFLM 297
 QY 202 QACRLKRCIYGVMMKGIKRDGRGRLMKHRRDDEGREGVSGADMRANLMPSPFLM 254
 Db 298 IKRSKNSLALSTADQVNSALDAEPP-LIYSEYDTPRPSPSEASMMGLTNLADREL 356
 QY 255 V-RELL-LD-ALSPDQLVTLLEAEPPVHLSR-PEAPTEASMMSLTKLADKELVH 308
 Db 357 MINNAKRVGFDVTLHDQVHLLCEGTEVLMIGLWRSMEHPVYKLFAPVLLDDRNGK 416
 QY 309 MIMNAKRVGFDVTLHDQVHLLCEGTEVLMIGLWRSMEHPVYKLFAPVLLDDRNGK 368
 Db 417 CVEGVEITFDMLATSSFRFMMNLOGEEFVCLTIILNSGVTFSLSTLSEEDKYI 476
 QY 369 CVEGVEITFDMLATSSFRFMMNLOGEEFVCLTIILNSGVTFSLSTLSEEDKYI 427
 Db 477 RVLDKTIIDTLIIMAKAGITLQOCHRRLAQOLLLSHRIHRSNKG 522
 QY 428 HLLNAVTDALVWTAKKGLTQOOSMRLANMLLSHVRAHSNKG 473
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 ID 091424 PRELIMINARY: PRT: 307 AA.
 AC 091424.
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE ESTROGEN RECEPTOR (FRAGMENT).
 OS CNEMIDOPHORUS UNIPARENS.
 OC EUKARYOTA; ANIMALIA; METAZOA; CHORDATA; VERTEBRATA; REPTILIA;
 OC LEPIDOSAURIA; SQUAMATA.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96103562.
 RA YOUNG L.J., GODWIN J., GRAMER M., GAHR M., CREWS D.;
 RL J. STEROID BIOCHEM. MOL. BIOL. 55:261-269(1995).
 DR EMBL; S79923; G1195592; -.
 DR PFAM; PF00104; hormone_rec.
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 FT NON_TER 1
 SQ SEQUENCE 307 AA; 35202 MW; DC0871D8 CRC32;

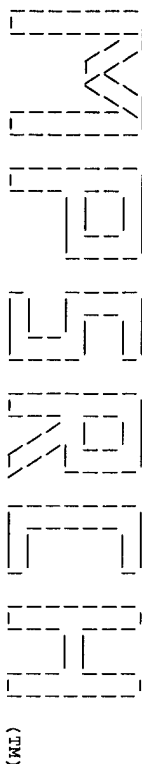
Query Match 31.4%; Score 1227; DB 13; Length 307;
 Best Local Similarity 56.7%; Pred. No. 1.08e-255;
 Matches 174; Conservative 68; Mismatches 53; Indels 12; Gaps 10;

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1 GHNDYACPATNOCTIDKNRRKSCQACRLKRCYEVGMKGIRKDRRGRIKHKRREEH 60
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QY 237 EQLHCAGKA--KRSGG--HAP-RV-RELLD-ALS--PEQLVTLTLEAEPHVLIS-RPSA 287
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Db 121 PFSEASMTLTLTLADRELVTMTNAKRYGFDLSLDQVHLLFCAMLEILMIGLYMRS 180
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 288 PFTASMMMSLTKLADKELVHMTSMACKIPGFVELSLFDQVRLLESCWMEVIMMGIMWRS 347
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 VEHGKILFAPNLLDNRNOCVEGFVEIFDMLATSRFRMNVQGEFVCLSIILN 240
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QY 348 IDHFGKLIAPDLVDRDEKCYEGILEIFDMLATSRFRKLQHKYELCYKAMILN 407
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QY 408 SSMTPLVTATODA-DSSRLAHLNVAFTDALVYVIAKSGISSQQSMRLANLMLLSHYR 466
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Db 301 HMSNKG 307
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QY 467 HASNKG 473

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Search completed: Mon Nov 2 16:36:13 1998
 Job time : 232 secs.



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MSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:36:30 1998; MasPar time 7.02 Seconds

Tabular output not generated. 534.685 Million cell updates/sec

Title: >US-08-906-365-2
Description: (1-530) from US08906365.pep
Perfect Score: 3904
Sequence: 1 MDIKNSPSSINSFSSYNCSQ.....ECSPAEDSKSKESQNSQ 530

Scoring table: PAM 150
Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 33.550; Variance 151.595; scale 0.221

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1648	42.2	410	3	5223606-5 Patent No. 5223606.	5.61e-141
2	660	16.9	363	3	5223606-6 Patent No. 5223606.	1.47e-48
3	609	15.6	356	3	5223606-7 Patent No. 5223606.	7.04e-44
4	577	14.8	795	1	US-07-716-Sequence 5, Applicatio	5.94e-41
5	539	13.6	533	1	US-07-952-Sequence 2, Applicatio	6.07e-37
6	533	13.7	446	1	US-07-952-Sequence 4, Applicatio	1.40e-36
7	514	13.2	467	1	US-08-336-Sequence 4, Applicatio	3.23e-35
8	514	13.2	467	2	PCT-US91-0-Sequence 4, Applicatio	3.23e-35
9	513	13.1	462	1	US-08-336-Sequence 2, Applicatio	3.98e-35
10	513	13.1	462	2	PCT-US91-0-Sequence 6, Applicatio	1.11e-32
11	466	12.4	463	1	US-08-336-Sequence 6, Applicatio	1.11e-32
12	466	12.4	463	2	PCT-US91-0-Sequence 6, Applicatio	1.11e-32
13	441	11.3	454	3	5260432-2 Patent No. 5260432.	1.27e-28
14	439	11.2	368	3	5223606-3 Patent No. 5223606.	1.91e-28
15	439	11.2	448	3	5223606-2 Patent No. 5223606.	1.91e-28
16	428	11.0	462	2	PCT-US92-0-Sequence 4, Applicatio	1.86e-27
17	428	11.0	797	2	PCT-US92-0-Sequence 8, Applicatio	9.69e-27
18	420	10.8	440	1	US-08-333-Sequence 8, Applicatio	9.69e-27
19	420	10.8	440	1	US-08-694-Sequence 8, Applicatio	9.69e-27
20	420	10.8	440	1	US-08-463-Sequence 8, Applicatio	9.69e-27
21	420	10.8	447	1	US-08-373-Sequence 8, Applicatio	9.69e-27
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26	365	9.3	348	1	US-08-459-Sequence 10, Applicati	7.68e-22
27	358	9.2	414	1	US-08-255-Sequence 9, Applicatio	3.20e-21
28	361	9.2	469	2	PCT-US95-1-Sequence 9, Applicatio	1.74e-21
29	357	9.1	89	1	US-08-087-Sequence 2, Applicatio	3.92e-21
30	357	9.1	89	1	US-08-561-Sequence 3, Applicatio	8.85e-21
31	353	9.0	484	2	PCT-US95-1-Sequence 1, Applicatio	8.85e-21
32	349	8.9	66	3	5217867-1 Patent No. 5217867.	2.00e-20
33	329	8.4	451	2	PCT-US95-1-Sequence 2, Applicatio	1.93e-18
34	315	8.1	70	1	US-07-737-Sequence 3, Applicatio	1.93e-17
35	307	7.9	443	1	US-08-342-Sequence 4, Applicatio	9.64e-17
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37	310	7.9	461	1	US-08-330-Sequence 2, Applicatio	5.28e-17
38	310	7.9	461	1	US-08-330-Sequence 2, Applicatio	5.28e-17
39	310	7.9	461	2	PCT-US95-1-Sequence 2, Applicatio	5.28e-17
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41	309	7.9	548	1	US-08-333-Sequence 2, Applicatio	6.45e-17
42	309	7.9	548	1	US-08-694-Sequence 2, Applicatio	6.45e-17
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ALIGNMENTS

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XX	01-JAN-1900				
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CC	Patent No. 5223606				
CC	APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLATS,				
CC	PIERRE; DEJEAN, ANNE				
CC	TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED				
CC	PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA				
CC	NUMBER OF SEQUENCES: 11				
CC	CURRENT APPLICATION NUMBER: US/07/134,130				
CC	APPLICATION NUMBER: US/07/134,130				
CC	FILING DATE: 17-DEC-1987				
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CC	LENGTH: 410				
CC	SEQUENCE 444 AA; 50020 MW; 1110634 CN;				

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Best Local Similarity 56.9%; Pred. No. 5.61e-141;
Matches 224; Conservative 92; Mismatches 64; Indels 14; Gaps 11;

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QY	318	GFVEISLFDQVRLBSCWHEVLMGMWRSIDHPGLIFAPVLDVDRGKVEGVETP	377
DB	241	DMILATSSRRFMANLQGEFFVLKSIILNSGVYTFSTLSLEKDIHVLDKITDY	300
QY	378	DMILATSSRRFMANLQGEFFVLKSIILNSGVYTFSTLSLEKDIHVLDKITDY	436

QY 327 QVRLLESCWMEVLMGMIMRSIDHPGKLIFAPDLYLDRECKVEGILEIFDMLLAT-TS 385

DB 356 KMRDMQMDKTELGCLRAIVLEPNPDSKGLSNPA-EVEA--L-R--EKVYASLE-AYCKHK 407

QY 386 RPELKLQHEEYLCVKAMILLNSMYPVLTATODDSRKLAHLINAVTALVWVIKSG 445

DB 408 YP-EQPG-RFARKLLRLPALRSIGKLEHLEFFFKLIGDTPIDTFLEMMEA 457

QY 446 ISSQOOSMRLANMLMLLSHVHRSNKGMEHLNMRCKNVVYDLEMLNA 497

RESULT 10
ID PCT-US91-00399-2 STANDARD; PRT; 462 AA.
XX xxxxxx

DE Sequence 2, Application PC/TUS9100399

CC GENERAL INFORMATION:
CC APPLICANT: Mangelsdorf, Dr., David J.
CC APPLICANT: Evans Dr., Ronald M.
CC TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND
CC TITLE OF INVENTION: METHODS
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
CC STREET: 135 South LaSalle Street, Suite 900
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/00399
CC FILING DATE: 19910122
CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/478,071
CC FILING DATE: 09-FEB-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Mr., Stephen E.
CC REGISTRATION NUMBER: 31192
CC REFERENCE/DOCKET NUMBER: 50852
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 552-1311
CC TELEFAX: (619) 552-0095
CC TELEX: 20 6566 PATLAW CGO
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 462 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 462 AA; 50811 MW; 1063517 CN;

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Best Local Similarity 33.0%; Pred. No. 3.98e-35;
Matches 116; Conservative 89; Mismatches 119; Indels 28; Gaps 21;

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QY 207 RRCYEVGWKVCGRRRRCGYRLVRRORSADDEOLHCGKAKRSQGNAPRYRELLIDALSP 266

DB 244 PRTIYVEANMG--L-N-PSSP-NDP--VTNICOADKOLFVLVEMAKRIPHFSELPDD 296

QY 267 QVLTLLLEAPPHVILSRSPAFTEBSMMSLTKLADKVLAMISMAKRIPFVELSLFD 326

DB 297 QVILLFAGNELLISFSRSTAVKDGILLATGALVHRSNASHA-GVGAIFRVLTELV 355

QY 327 QVRLLESCWMEVLMGMIMRSIDHPGKLIFAPDLYLDRECKVEGILEIFDMLLAT-TS 385

DB 356 KMRDMQMDKTELGCLRAIVLEPNPDSKGLSNPA-EVEA--L-R--EKVYASLE-AYCKHK 407

QY 386 RPELKLQHEEYLCVKAMILLNSMYPVLTATODDSRKLAHLINAVTALVWVIKSG 445

DB 408 YP-EQPG-RFARKLLRLPALRSIGKLEHLEFFFKLIGDTPIDTFLEMMEA 457

QY 446 ISSQOOSMRLANMLMLLSHVHRSNKGMEHLNMRCKNVVYDLEMLNA 497

RESULT 11
ID US-08-336-408B-6 STANDARD; PRT; 463 AA.
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DE Sequence 6, Application US/08336408B

CC GENERAL INFORMATION:
CC APPLICANT: MANGELSDORF, DAVID J.
CC APPLICANT: EVANS, RONALD M.
CC TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND
CC TITLE OF INVENTION: METHODS
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
CC STREET: 444 SOUTH FLOWER STREET, SUITE 2000
CC CITY: LOS ANGELES
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 90071

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/336,408B
CC FILING DATE: 08-NOV-1994
CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/933,453
CC FILING DATE: 21-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: WO PCT/US91/00399
CC FILING DATE: 22-JAN-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/478,071
CC FILING DATE: 09-FEB-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: REITER, STEPHEN E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: P41 9851
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-546-1995
CC TELEFAX: 619-546-9392
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 463 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein


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QY 329 RLL-ESCWMEVLMGLMMSRIDHPGKLIIFAPDLVLDREKCYEGILIEIFDMLATTSRF 387
DB 319 LPLEMDTE---TG--LL-SALICIGDRMDLEEPKVDKLOEPLEAL-RLYARRRRP 370
QY 388 RELKLOHKEYLCYKAMILLNMSMYPLVATQDADSSKRLAHNLNAVYDALVWVIKSGIS 447
DB 371 SQP-YM-FPRLMKITDRLGISTGAEARITLKMELIPGMPPLIREMLE 417
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RESULT 14
ID 5223606-3 STANDARD; PRT; 398 AA.
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AC xxxxxx
XX
DT 01-JAN-1900
DE Patent No. 5223606.
XX
CC Patent No. 5223606
CC APPLICANT: BLAUDIN DE THE, HUGHES;MARCHIO, AGNES;TIOUAIIS,
CC PIERRE;DEJEAN, ANNE
CC TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
CC PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
CC NUMBER OF SEQUENCES: 11
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/134,130
CC FILING DATE: 17-DEC-1987
CC PRIOR APPLICATION DATA:
CC SEQ ID NO:3:
CC LENGTH: 368
CC SEQUENCE 398 AA; 44842 MM; 907111 CN;

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Best Local Similarity 26.9%; Pred. No.1,91e-28;
Matches 94; Conservative 97; Mismatches 136; Indels 22; Gaps 18;

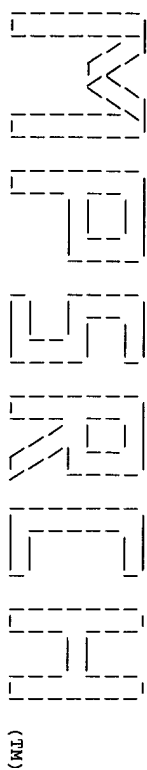
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QY 209 CFEVGVKCGSRREGCYRLVRQRORSADEQLHCAGKAKRSGHAPRYRELLDALSPEDL 268
DB 116 C-QL-GKYTTNSSADHR-VOL-DGLMDKFSELATCIIIVEFAKRLPGFTGLTADQI 171
QY 269 VLTLLAEPPHYLISRPASFTESMMMSLTKLADKELVHMISWAKKIPGFVLSLFDQY 328
DB 172 TLTKAAC-LDILILRICRTYTPEDDTMFSDGLTLNRTQ-MHNAGFPLDVFAPAGOL 229
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DB 230 LPLEMDTE---TG--LL-SALICIGDRMDLEEPKVDKLOEPLEAL-RLYARRRRP 281
QY 388 RELKLOHKEYLCYKAMILLNMSMYPLVATQDADSSKRLAHNLNAVYDALVWVIKSGIS 447
DB 282 SKPH-M-FPKILMKITDRLGISTGAEARITLKMELIPGMPPLIREMLE 328
QY 448 SQOOSMRLANLMLLSHVHRASNKGMHLLNMCKKNVVPYDILLEMLN 496
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RESULT 15
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AC xxxxxx
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DT 01-JAN-1900
DE Patent No. 5223606.
XX
CC Patent No. 5223606
CC APPLICANT: BLAUDIN DE THE, HUGHES;MARCHIO, AGNES;TIOUAIIS,
CC PIERRE;DEJEAN, ANNE
CC TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
CC PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
CC NUMBER OF SEQUENCES: 11
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/134,130
CC FILING DATE: 17-DEC-1987
CC PRIOR APPLICATION DATA:
CC SEQ ID NO:2:
CC LENGTH: 448
CC SEQUENCE 485 AA; 54437 MM; 1345912 CN;

Query Match 11.2%; Score 439; DB 3; Length 448;
Best Local Similarity 26.9%; Pred. No.1,91e-28;
Matches 94; Conservative 97; Mismatches 136; Indels 22; Gaps 18;

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DB 362 SKPH-M-FPKILMKITDRLGISTGAEARITLKMELIPGMPPLIREMLE 408
QY 448 SQOOSMRLANLMLLSHVHRASNKGMHLLNMCKKNVVPYDILLEMLN 496

Search completed: Mon Nov 2 16:37:14 1998
Job time : 44 secs.
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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:15:30 1998; MasPar time 2128.26 Seconds

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Comp: gtcggtatattgacgggtg.....tcttggtgacgagtcact

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Gap 6

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Searched: 1988617 segs, 767163441 bases x 2

Post-processing: Minimum Match 0%
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3:gb-est1 4:gb-est10 5:gb-est11 6:gb-est12 7:gb-est13
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12:gb-est18 13:gb-est19 14:gb-est20 15:gb-est21
16:gb-est22 17:gb-est23 18:gb-est24 19:gb-est25
20:gb-est26 21:gb-est27 22:gb-est28 23:gb-est29 24:gb-est30
25:gb-est31 26:gb-est32 27:gb-est33

Statistics: Mean 11.528; Variance 1.960; scale 5.882

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	173	10.3	531	15	AA224131	0.00e+00
2	76	4.5	466	13	AA744644	2.42e-105
3	68	4.0	252	13	AA754459	4.00e-88
4	63	3.7	252	13	AA754459	1.46e-77
5	61	3.6	534	7	AA517920	2.19e-73
6	56	3.3	384	16	AA893618	4.37e-63
7	56	3.3	384	16	AA851319	4.37e-63
8	52	3.1	247	13	AA754458	5.21e-55
9	52	3.1	390	10	W13715	5.21e-55
10	52	3.1	403	21	H91890	5.21e-55
11	53	3.1	454	21	H82542	5.16e-57
12	53	3.1	462	5	AA411385	5.16e-57
13	50	3.0	280	16	AA876157	4.93e-51

14	51	3.0	412	24	AA157597	5.13e-53
15 <td>48 <td>2.8 <td>508 <td>23 <td>W53545 <td>4.19e-47 </td></td></td></td></td></td>	48 <td>2.8 <td>508 <td>23 <td>W53545 <td>4.19e-47 </td></td></td></td></td>	2.8 <td>508 <td>23 <td>W53545 <td>4.19e-47 </td></td></td></td>	508 <td>23 <td>W53545 <td>4.19e-47 </td></td></td>	23 <td>W53545 <td>4.19e-47 </td></td>	W53545 <td>4.19e-47 </td>	4.19e-47
16 <td>48 <td>2.8 <td>536 <td>23 <td>AA003987 <td>4.19e-47 </td></td></td></td></td></td>	48 <td>2.8 <td>536 <td>23 <td>AA003987 <td>4.19e-47 </td></td></td></td></td>	2.8 <td>536 <td>23 <td>AA003987 <td>4.19e-47 </td></td></td></td>	536 <td>23 <td>AA003987 <td>4.19e-47 </td></td></td>	23 <td>AA003987 <td>4.19e-47 </td></td>	AA003987 <td>4.19e-47 </td>	4.19e-47
17 <td>47 <td>2.8 <td>653</td> <td>13 <td>AA1073549 <td>3.70e-45 </td></td></td></td></td>	47 <td>2.8 <td>653</td> <td>13 <td>AA1073549 <td>3.70e-45 </td></td></td></td>	2.8 <td>653</td> <td>13 <td>AA1073549 <td>3.70e-45 </td></td></td>	653	13 <td>AA1073549 <td>3.70e-45 </td></td>	AA1073549 <td>3.70e-45 </td>	3.70e-45
18 <td>46 <td>2.7 <td>247</td> <td>13 <td>AA754458 <td>3.18e-43 </td></td></td></td></td>	46 <td>2.7 <td>247</td> <td>13 <td>AA754458 <td>3.18e-43 </td></td></td></td>	2.7 <td>247</td> <td>13 <td>AA754458 <td>3.18e-43 </td></td></td>	247	13 <td>AA754458 <td>3.18e-43 </td></td>	AA754458 <td>3.18e-43 </td>	3.18e-43
19 <td>46 <td>2.7 <td>479</td> <td>13 <td>AA821160 <td>3.18e-43 </td></td></td></td></td>	46 <td>2.7 <td>479</td> <td>13 <td>AA821160 <td>3.18e-43 </td></td></td></td>	2.7 <td>479</td> <td>13 <td>AA821160 <td>3.18e-43 </td></td></td>	479	13 <td>AA821160 <td>3.18e-43 </td></td>	AA821160 <td>3.18e-43 </td>	3.18e-43
20 <td>42 <td>2.5 <td>616</td> <td>17 <td>AA886743 <td>1.24e-35 </td></td></td></td></td>	42 <td>2.5 <td>616</td> <td>17 <td>AA886743 <td>1.24e-35 </td></td></td></td>	2.5 <td>616</td> <td>17 <td>AA886743 <td>1.24e-35 </td></td></td>	616	17 <td>AA886743 <td>1.24e-35 </td></td>	AA886743 <td>1.24e-35 </td>	1.24e-35
21 <td>41 <td>2.4 <td>552</td> <td>23 <td>W53477 <td>8.98e-34 </td></td></td></td></td>	41 <td>2.4 <td>552</td> <td>23 <td>W53477 <td>8.98e-34 </td></td></td></td>	2.4 <td>552</td> <td>23 <td>W53477 <td>8.98e-34 </td></td></td>	552	23 <td>W53477 <td>8.98e-34 </td></td>	W53477 <td>8.98e-34 </td>	8.98e-34
22 <td>40 <td>2.4 <td>593</td> <td>25 <td>AA023625 <td>6.24e-32 </td></td></td></td></td>	40 <td>2.4 <td>593</td> <td>25 <td>AA023625 <td>6.24e-32 </td></td></td></td>	2.4 <td>593</td> <td>25 <td>AA023625 <td>6.24e-32 </td></td></td>	593	25 <td>AA023625 <td>6.24e-32 </td></td>	AA023625 <td>6.24e-32 </td>	6.24e-32
23 <td>38</td> <td>2.3 <td>365</td> <td>24 <td>AA092184 <td>2.66e-28 </td></td></td></td>	38	2.3 <td>365</td> <td>24 <td>AA092184 <td>2.66e-28 </td></td></td>	365	24 <td>AA092184 <td>2.66e-28 </td></td>	AA092184 <td>2.66e-28 </td>	2.66e-28
24 <td>38</td> <td>2.3 <td>393</td> <td>14 <td>R52304 <td>2.66e-28 </td></td></td></td>	38	2.3 <td>393</td> <td>14 <td>R52304 <td>2.66e-28 </td></td></td>	393	14 <td>R52304 <td>2.66e-28 </td></td>	R52304 <td>2.66e-28 </td>	2.66e-28
25 <td>38</td> <td>2.3 <td>604</td> <td>25 <td>AA049907 <td>2.66e-28 </td></td></td></td>	38	2.3 <td>604</td> <td>25 <td>AA049907 <td>2.66e-28 </td></td></td>	604	25 <td>AA049907 <td>2.66e-28 </td></td>	AA049907 <td>2.66e-28 </td>	2.66e-28
26 <td>36</td> <td>2.1 <td>289</td> <td>5 <td>AA382009 <td>9.45e-25 </td></td></td></td>	36	2.1 <td>289</td> <td>5 <td>AA382009 <td>9.45e-25 </td></td></td>	289	5 <td>AA382009 <td>9.45e-25 </td></td>	AA382009 <td>9.45e-25 </td>	9.45e-25
27 <td>36</td> <td>2.1 <td>532</td> <td>16 <td>AA799413 <td>9.45e-25 </td></td></td></td>	36	2.1 <td>532</td> <td>16 <td>AA799413 <td>9.45e-25 </td></td></td>	532	16 <td>AA799413 <td>9.45e-25 </td></td>	AA799413 <td>9.45e-25 </td>	9.45e-25
28 <td>36</td> <td>2.1 <td>566</td> <td>23 <td>W53511 <td>9.45e-25 </td></td></td></td>	36	2.1 <td>566</td> <td>23 <td>W53511 <td>9.45e-25 </td></td></td>	566	23 <td>W53511 <td>9.45e-25 </td></td>	W53511 <td>9.45e-25 </td>	9.45e-25
29 <td>36</td> <td>2.1 <td>646</td> <td>7 <td>AA543722 <td>9.45e-25 </td></td></td></td>	36	2.1 <td>646</td> <td>7 <td>AA543722 <td>9.45e-25 </td></td></td>	646	7 <td>AA543722 <td>9.45e-25 </td></td>	AA543722 <td>9.45e-25 </td>	9.45e-25
30 <td>36</td> <td>2.1 <td>700</td> <td>11 <td>AA673643 <td>9.45e-25 </td></td></td></td>	36	2.1 <td>700</td> <td>11 <td>AA673643 <td>9.45e-25 </td></td></td>	700	11 <td>AA673643 <td>9.45e-25 </td></td>	AA673643 <td>9.45e-25 </td>	9.45e-25
31 <td>33</td> <td>2.0 <td>404</td> <td>11 <td>AA675734 <td>1.36e-19 </td></td></td></td>	33	2.0 <td>404</td> <td>11 <td>AA675734 <td>1.36e-19 </td></td></td>	404	11 <td>AA675734 <td>1.36e-19 </td></td>	AA675734 <td>1.36e-19 </td>	1.36e-19
32 <td>34</td> <td>2.0 <td>460</td> <td>5 <td>AA401262 <td>2.74e-21 </td></td></td></td>	34	2.0 <td>460</td> <td>5 <td>AA401262 <td>2.74e-21 </td></td></td>	460	5 <td>AA401262 <td>2.74e-21 </td></td>	AA401262 <td>2.74e-21 </td>	2.74e-21
33 <td>34</td> <td>2.0 <td>471</td> <td>10 <td>AA428473 <td>2.74e-21 </td></td></td></td>	34	2.0 <td>471</td> <td>10 <td>AA428473 <td>2.74e-21 </td></td></td>	471	10 <td>AA428473 <td>2.74e-21 </td></td>	AA428473 <td>2.74e-21 </td>	2.74e-21
34 <td>32</td> <td>1.9 <td>378</td> <td>6 <td>C08482 <td>6.32e-18 </td></td></td></td>	32	1.9 <td>378</td> <td>6 <td>C08482 <td>6.32e-18 </td></td></td>	378	6 <td>C08482 <td>6.32e-18 </td></td>	C08482 <td>6.32e-18 </td>	6.32e-18
35 <td>31</td> <td>1.8 <td>303</td> <td>4 <td>AA351366 <td>2.77e-16 </td></td></td></td>	31	1.8 <td>303</td> <td>4 <td>AA351366 <td>2.77e-16 </td></td></td>	303	4 <td>AA351366 <td>2.77e-16 </td></td>	AA351366 <td>2.77e-16 </td>	2.77e-16
36 <td>31</td> <td>1.8 <td>338</td> <td>5 <td>AA373868 <td>2.77e-16 </td></td></td></td>	31	1.8 <td>338</td> <td>5 <td>AA373868 <td>2.77e-16 </td></td></td>	338	5 <td>AA373868 <td>2.77e-16 </td></td>	AA373868 <td>2.77e-16 </td>	2.77e-16
37 <td>30</td> <td>1.8 <td>446</td> <td>13 <td>AA822242 <td>1.13e-14 </td></td></td></td>	30	1.8 <td>446</td> <td>13 <td>AA822242 <td>1.13e-14 </td></td></td>	446	13 <td>AA822242 <td>1.13e-14 </td></td>	AA822242 <td>1.13e-14 </td>	1.13e-14
38 <td>30</td> <td>1.8 <td>2275</td> <td>11 <td>AF034173 <td>1.13e-14 </td></td></td></td>	30	1.8 <td>2275</td> <td>11 <td>AF034173 <td>1.13e-14 </td></td></td>	2275	11 <td>AF034173 <td>1.13e-14 </td></td>	AF034173 <td>1.13e-14 </td>	1.13e-14
39 <td>29</td> <td>1.7 <td>163</td> <td>3 <td>T83788 <td>4.29e-13 </td></td></td></td>	29	1.7 <td>163</td> <td>3 <td>T83788 <td>4.29e-13 </td></td></td>	163	3 <td>T83788 <td>4.29e-13 </td></td>	T83788 <td>4.29e-13 </td>	4.29e-13
40 <td>28</td> <td>1.7 <td>200</td> <td>11 <td>AA679591 <td>1.51e-11 </td></td></td></td>	28	1.7 <td>200</td> <td>11 <td>AA679591 <td>1.51e-11 </td></td></td>	200	11 <td>AA679591 <td>1.51e-11 </td></td>	AA679591 <td>1.51e-11 </td>	1.51e-11
41 <td>29</td> <td>1.7 <td>240</td> <td>9 <td>C39610 <td>4.29e-13 </td></td></td></td>	29	1.7 <td>240</td> <td>9 <td>C39610 <td>4.29e-13 </td></td></td>	240	9 <td>C39610 <td>4.29e-13 </td></td>	C39610 <td>4.29e-13 </td>	4.29e-13
42 <td>28</td> <td>1.7 <td>431</td> <td>23 <td>AA044343 <td>1.51e-11 </td></td></td></td>	28	1.7 <td>431</td> <td>23 <td>AA044343 <td>1.51e-11 </td></td></td>	431	23 <td>AA044343 <td>1.51e-11 </td></td>	AA044343 <td>1.51e-11 </td>	1.51e-11
43 <td>28</td> <td>1.7 <td>578</td> <td>23 <td>W74889 <td>1.51e-11 </td></td></td></td>	28	1.7 <td>578</td> <td>23 <td>W74889 <td>1.51e-11 </td></td></td>	578	23 <td>W74889 <td>1.51e-11 </td></td>	W74889 <td>1.51e-11 </td>	1.51e-11
44 <td>29</td> <td>1.7 <td>628</td> <td>18 <td>A1037274 <td>4.29e-13 </td></td></td></td>	29	1.7 <td>628</td> <td>18 <td>A1037274 <td>4.29e-13 </td></td></td>	628	18 <td>A1037274 <td>4.29e-13 </td></td>	A1037274 <td>4.29e-13 </td>	4.29e-13
45 <td>29</td> <td>1.7 <td>2275</td> <td>11 <td>AF034173 <td>4.29e-13 </td></td></td></td>	29	1.7 <td>2275</td> <td>11 <td>AF034173 <td>4.29e-13 </td></td></td>	2275	11 <td>AF034173 <td>4.29e-13 </td></td>	AF034173 <td>4.29e-13 </td>	4.29e-13

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCSSION	NID	KEYWORDS	SOURCE	ORGANISM
1	AA224131	531 bp mRNA	AA224131	g1844690	EST.	human.	Homo sapiens
	z14e02.r1	Stratagene hnt neuron (#937233)					Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 531)	Hillier, L., Allen, M., Bowles, L., Dubugre, T., Giesel, G., Jost, S., Martin, J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.	WashU-NCI human EST Project	Unpublished (1997)	Contact: Wilson R Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu

High quality sequence stop: 357.
Location/Qualifiers
1. 531
/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectional. Primer: Oligo dT. Differentiated, post mitotic hnt neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'

GAATTCGCGACGAG 3' -3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTT 3',"
 /db.xref="GDB:5589314"
 /db.xref="taxon:9606"
 /clone="648794"
 /clone_lib="Stratagene hnt neuron (#937233)"
 /dev_stage="hnt neurons"
 /lab_host="SOLR (kanamycin resistant)"
 BASE COUNT 192 a 74 c 112 g 146 t 7 others
 ORIGIN

Query Match 10.3%; Score 173; DB 15; Length 531;
 Best Local Similarity 99.4%; Pred. No. 0.00e+00;
 Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 27 CGTGTCCAGGGGTAGATGATGATGCTGAGTGTAGAGAGAAGATTAAGCTAG 86
 Cp 175 cgtgtccaggggtaagatgagatgactgcagctgtgagagagaagaaatagagctag 116
 Db 87 ATGCTGAGTTTTTATATCCATGCTGTGAGATACAGCTGAGAAAACACCTTGCAAGAAG 146
 Cp 115 atgtgagttttttatatacatgctgtgagatgacgtgagaaaacaccttgcaagaag 56
 Db 147 AGGCACAAAGTCATATATATGTTCTCAAGATTCGTGGCAGCATATATGCTG 201
 Cp 55 aggcacaaagtcataataatgcttccaaagatcgtggcagatgataatgctg 1

RESULT 2 AA744644 466 bp mRNA EST 07-FEB-1998
 LOCUS n79f02.s1 NCI-CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1284507
 DEFINITION similar to gb:MI2674 ESTROGEN RECEPTOR (HUMAN);, mRNA sequence.
 ACCESSION AA744644
 NID 92783408
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 466)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Insert length: 1369 Std Error: 0.00
 Seg primer: -40m3 fwd. ET from Amersham
 High quality sequence stop: 430.
 Location/Qualifiers
 1. 466
 /organism="Homo sapiens"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCCGCCCTCATTTTCTTTTCTTTT-
 3']. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p773 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 /db.xref="taxon:9606"
 /clone="IMAGE:1284507"
 /clone_lib="NCI-CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 BASE COUNT 113 a 134 c 130 g 88 t 1 others
 ORIGIN

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 Matches 96; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Db 351 GGAGCTGGTCTCTGAGGCGTCGAAGCCTCTTCAGAGAAGATTCAGACATAAC 410
 Qy 577 ggaagctggctctgagaggaatgtaagccttttaagaagaagatcaagacataat 636
 Db 411 GACTATATGTGTCAGCCACCAACGATGACCATTTGATTAAGAAGAGAAGAG 466
 Qy 637 gattatattgtccagctacataatcagtgtaacatcgataaaccgcgcagaag 692

RESULT 3 AA754459 252 bp mRNA EST 20-JAN-1998
 LOCUS 97SN1787 Rice Immature Seed Lambda ZAPII cDNA library Oryza sativa
 DEFINITION cDNA clone 97SN1787, mRNA sequence.
 ACCESSION AA754459
 NID 92801165
 KEYWORDS EST.
 SOURCE rice.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.
 REFERENCE 1 (bases 1 to 252)
 AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
 Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
 Lee,M.C. and Eun,M.Y.
 TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 JOURNAL Unpublished (1998)
 COMMENT

Contact: Eun M.Y.
 Department of Cyto genetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggi-do, Korea
 Tel: 82 331 290 0301
 Fax: 82 331 290 0307
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 Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 binaim@ioserver.myongji.ac.kr
 Seq primer: M13 Reverse Primer.
 Location/Qualifiers
 1. 252
 /organism="Oryza sativa"
 /cultivar="Milyang23"
 /note="Vector: phuescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Directional cDNA library inserted into lambda ZAPII
 vector at 5' end with EcoRI and 3' end with Xho I site."
 /db.xref="taxon:4530"
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 /tissue_type="Immature Seed"
 /dev_stage="5 days after pollination"
 /lab_host="E. coli SOLR"

BASE COUNT 5 a 21 c 12 g 35 t 179 others
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 Best Local Similarity 11.8%; Pred. No. 4.00e-88;
 Matches 27; Conservative 123; Mismatches 75; Indels 4; Gaps 3;

OY	983	ccgcagcaagtgtccgacaaagaagtgtgtacacatgatcagctggcccgaagaatttc	1042
Db	127	BMBBTGCTCTTMCQWBHYNFKCTASGHNISTNDVKSSTTWGTBYSDXSMHGTC	186
OY	1043	ccgactgtttagagctcagccctgttcgaccacaagtgagcgctcttggagagcttgtgattg	1102
Db	187	BVKHTKVTSTRANRS-YTCVRKYCVMMMTKKYVKKHVBGBCHBMDSCCKTKMMTK	244
OY	1103	aggctctaatagtatggcgctgctgtgcgcacctaatgacaccccgcaagctcatctt	1161
RESULT	5	AA517920	534 bp mRNA EST 14-JUL-1997
LOCUS		vhp95e40.r1 Barstead mouse myotubes MRLRB5 Mus musculus cDNA clone	
DEFINITION		902038 5' similar to gb:M4446 Mouse retinolic acid receptor gamma	
ACCESSION		(MUSE); mRNA sequence.	
NID		AA517920	
KEYWORDS		G2257444	
SOURCE		EST.	
ORGANISM		house mouse.	
		Mus musculus	
		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;	
		Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;	
		Murinae; Mus.	
REFERENCE		1 (bases 1 to 534)	
AUTHORS		Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Weisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Weston,R.	
TITLE		The WashU-HMI Mouse EST Project	
JOURNAL		Unpublished (1996)	
COMMENT		Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:522722 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 393. Location/Qualifiers 1. 534 /organism="Mus musculus" /strain="C3H" /note="vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site.1: EcoRI; Site.2: NotI; 1st strand cDNA was primed with a Not I - oligo(dAT) primer [5' TGTTAGCAATCTGAAGCGAGGGCCGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTGGCATCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRJ-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins." /db_xref="taxon:10090" /clone_1="902058" /clone_1lb="Barstead mouse myotubes MRLRB5" /cell_line="C2C12" /lab_host="DH10B" <1. .2534	
BASE COUNT	128 a	153 c	143 g 110 t
ORIGIN	mRNA		
Query Match	3.6%	Score 61:	DB 7: Length 534;
Best Local Similarity	66.7%;	Pred. No. 2.19e-73;	
Matches	132; Conservative	0; Mismatches 65;	Indels 1; Gaps 1;

Db	315	TCGCTTGATGCAAGAAAGCTTCTGGCTACACATGAGGGGTGACGTCCTGTGAAGGC	374
Qy	538	tcgcgtgtcgtgaagsgattacgcacatcgcgatatacctatgagcttgcgtgtgaaaga	597
Db	375	TGCAAGGGCTTCTTGACAGCAGCATTCAGAGAAACATGGTGATATACATGTACCGTGACA	434
Qy	538	tgtaaagccctttttaaagaagcattcaagaagacataatgatatattatgttcocagctaca	657
Db	435	AAA-ACTGATATATCAACAAGGTCAACGAAATGCATGCCAGTACTGCAGGCTACAAAG	493
Qy	658	aatcgtgtgacatcgtataataaaacccgcgcagaagctgccagcctgcgcgacttcggaag	717
Db	494	TGTTTCGAAGTGGCGATG	511
Qy	718	tgttacgaagtgtggaatg	735
RESULT	6		
LOCUS	AA893618	384 bp	mRNA
DEFINITION	ESR197421 Normalized rat placenta, Bento Soares Rattus sp. cDNA		
ACCESSION	AA893618		
NID	93020497		
KEYWORDS	EST.		
SOURCE	Rattus sp.		
ORGANISM	Rattus sp.		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.		
TITLE	Rat Genome Project: Generation of a Rat EST (RER) Catalog & Rat Gene Index		
JOURNAL	Unpublished (1998)		
COMMENT			
	Contact: Lee, NH		
	ATCC		
	The Institute for Genomic Research		
	9712, Medical Center Drive, Rockville, MD 20850, USA		
	Tel: (301)-838-3529		
	Fax: (301)-838-0208		
	Email: nhlee@tigr.org		
FEATURES			
Source	Location/Qualifiers		
	1..384		
	/organism="Rattus sp."		
	/note="Organ: placenta; Vector: pT7mpac; Site_1: EORI		
	Site_2: NotI"		
	/db_xref="taxon:10118"		
	/clone="RPLC64"		
	/clone_id="Normalized rat placenta, Bento Soares"		
BASE COUNT	87 a 102 c 94 g 101 t		
ORIGIN			
Query Match	3.3%; Score 56; DB 16; Length 384;		
Best Local Similarity	64.0%; Pred. No. 4.37e-63;		
Matches	128; Conservative 0; Mismatches 72; Indels 0; Gaps 0;		
Db	15	CATTCACGCCCTGGAAGACATTTCCGATACGGCAGTCGGAGTTTTCCTCGAATTTT	74
Cp	735	cattccacccttcgtaaacctccgaagtcggaagcctgtgacgcttgcgcggttttc	676
Db	75	ATCAATGATGCAATCGTTTCTTCACAGCAAAAGGTAATGTGCTGCTCCATCGCTCT	134
Cp	675	atcgatgtacacgattgtgtagctgtgacaaatataatcatatgcttcgtgaatgcttc	616
Db	135	TTTAAAGAAATCTTTGACAGCTTCCATGTCAGCAACCCCGTAATGACCTGAGCTTC	194
Cp	615	tttaaaaaggccttacctccttcacacgaccagatcctatagatataccgatgcta	556
Db	195	ATCGAGCACCAAGGACA	214
Cp	555	atcgctcgacagacgcgaca	536

RESULT	7	AA851319	384 bp	mRNA	EST	30-APR-1998
DEFINITION	EST194087	Normalized rat placenta, Bento Soares Rattus sp. cDNA clone RP1AF19 3' end, mRNA sequence.				
ACCESSION	AA851319					
NID	92938859					
KEYWORDS	EST.					
SOURCE	Rattus sp.					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (bases 1 to 384)					
AUTHORS	Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J., Karlavage,A.R. and Adams,M.D.					
TITLE	Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat Gene Index					
JOURNAL	Unpublished (1998)					
COMMENT	Contact: Lee, NH ATCC The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.					
FEATURES	Location/Qualifiers					
SOURCE	1..384 /organism="Rattus sp." /note="Organ: placenta; Vector: pT73Pac; site_1: EcoRI; site_2: NotI" /db_xref="ATCC (inhost):2011237" /db_xref="taxon:10118" /clone="RP1AF19" /clone_1ib="Normalized rat placenta, Bento Soares" BASE COUNT 87 a 102 c 94 g 101 t					
ORIGIN						
Query Match	3.3%; Score 56; DB 16; Length 384;					
Best Local Similarity	64.0%; Pred. No. 4.37e-63;					
Matches 128; Conservative	0; Mismatches 72; Indels 0; Gaps 0;					
Db	15	CATTCCAGCCTGAAGACATTTCCGATAGGGGATGCTGGCAGTTTTCCTCGAATTT	74			
Cp	735	catccacacttcgtaaacacttcggaagtcgagcgccctgcagctcttcgcgcggttttt	676			
Db	75	ATCATGATGCATGCTTTCTTTCACACAGAAGTATGTGCTGCTTCCTCCACGCTCT	134			
Cp	675	atcgatctgacactgattctgttagctgagcaaatatcatatctatgctctgaatgctct	616			
Db	135	TTTAAAGATACTTTTCAGGCTTCACATGTCAGCACCCCGTATGACATCCTGAAGTTTC	194			
Cp	615	tttataaagcgcttcatccttcacaacagcagcagctcatatgatatcccgatgogta	556			
Db	195	ATCGGAGCACACACGACGACGA 214				
Cp	555	atcgctgcagacagcgacga 536				
RESULT	8	AA754458	247 bp	mRNA	EST	20-JAN-1998
LOCUS						
DEFINITION	97SN1784	Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa				
ACCESSION	AA754458					
NID	92801164					
KEYWORDS	EST.					
SOURCE	rice					
ORGANISM	Oryza sativa					
	Eukaryota; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.					

(TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Nov 2 16:24:20 1998; MasPar time 20.72 Seconds
Tabular output not generated. 413.984 Million cell updates/sec

Title: >US-08-906-365-2
Description: (1-530) from US08906365.pep
Perfect Score: 3904
Sequence: 1 MDIKNSPSSLNPSSTSYNCQ.....ECSPADSKSKREGSONPOQO 530

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a.geneseq32
1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 36.033; Variance 154.129; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3904	100.0	530 28	W33215	Human oestrogen recep	0.00e+00
2	3582	91.8	485 21	W14774	Human oestrogen recep	0.00e+00
3	3532	90.5	477 28	W33212	Human oestrogen recep	0.00e+00
4	3274	83.9	485 21	W14773	Rat oestrogen recepto	0.00e+00
5	3250	83.2	485 21	W14725	Mouse oestrogen recep	0.00e+00
6	3099	79.4	416 27	W33213	Human oestrogen recep	4.32e-293
7	3099	79.4	418 28	W33214	Human oestrogen recep	4.32e-293
8	1714	43.9	233 27	W33211	Human oestrogen recep	2.24e-154
9	1671	42.8	595 2	P70543	Human oestrogen recep	4.30e-150
10	1424	36.5	334 2	P80925	Sequence of the human	1.58e-125
11	807	20.7	433 2	P80931	Sequence of human est	1.04e-64
12	800	20.5	521 2	P80930	Sequence of human est	5.02e-64
13	614	15.7	777 2	P80919	Sequence of the prima	5.47e-46
14	614	15.7	777 28	W44700	Mutant nuclear glucoc	5.47e-46
15	590	15.1	1070 23	W17789	Green fluorescent pro	1.11e-43
16	576	14.8	902 3	R12224	Rat androgen receptor	2.46e-42
17	570	14.6	902 1	P93110	Rat androgen receptor	9.28e-42
18	570	14.6	902 1	P91006	Rat androgen receptor	9.28e-42

19	570	14.6	918 3	R12223	Human androgen recept	9.28e-42
20	567	14.5	919 22	W14783	Androgen receptor.	1.80e-41
21	567	14.5	919 1	P90996	Human androgen recept	1.80e-41
22	566	14.5	919 1	P93109	Human androgen recept	2.24e-41
23	563	14.4	77 10	R53289	Human oestrogen recep	4.35e-41
24	546	14.0	72 1	P91994	Part of oestrogen rec	1.85e-39
25	545	14.0	630 3	R12230	TYPE/androgen recepto	2.30e-39
26	535	13.7	66 28	W33210	Human oestrogen recep	2.08e-38
27	536	13.7	68 13	R15666	Human oestrogen recep	1.67e-38
28	533	13.7	533 8	R39468	Partial human estroge	3.23e-38
29	533	13.7	533 13	R72483	Human H-2RIIBP.	3.22e-38
30	529	13.6	446 6	R11837	H2RIIBP nuclear hormo	7.79e-38
31	529	13.6	446 13	R21844	H-2RIIBP.	7.79e-38
32	528	13.5	510 8	R39469	hRXR-beta2.	9.70e-38
33	525	13.4	448 8	R39467	hRXR-beta.	1.88e-37
34	521	13.3	984 2	P80927	Sequence of the human	4.52e-37
35	514	13.2	467 8	R39470	hRXR-alpha.	2.10e-36
36	514	13.2	467 3	R13799	Human RXR-alpha retin	2.10e-36
37	509	13.0	462 3	R13798	Human RXR-alpha retin	5.03e-34
38	489	12.5	463 8	R39471	Mouse RXR-gamma.	9.69e-34
39	486	12.4	463 3	R13800	Human RXR-gamma retin	1.66e-32
40	473	12.1	463 20	W00605	Human retinoid X rece	2.57e-32
41	471	12.1	598 9	R48631	Sequence of nuclear r	3.09e-30
42	449	11.5	447 4	R20466	Mouse retinoic acid r	2.49e-30
43	450	11.5	458 2	R10549	Skin-specific murine	3.09e-30
44	449	11.5	458 4	R20465	Mouse retinoic acid r	4.77e-30
45	447	11.4	438 23	W18033	Zebrafish retinoid X	

ALIGNMENTS

RESULT 1
ID W33215 standard; Protein; 530 AA.

AC	W33215; 1998 (first entry)
DE	Human oestrogen receptor protein #2.
KW	Oestrogen receptor protein; steroid; alternative splicing; estradiol;
KW	estosterone; estrinol; screening.
OS	Homo sapiens
PN	EP-798376-A2.
PF	01-OCT-1997.
PR	25-MAR-1997; 200903.
PR	22-NOV-1996; EP-203284.
PR	26-MAR-1996; EP-200820.
PA	(ALKU) AKZO NOBEL NV.
PI	Dijkema R, Mosselman S;
DR	WPI; 97-473188/44.
DR	N-PSDB; T88415.
PT	DNA encoding estrogen receptor - useful in screening assay to
PT	identify novel ligands or hormonal analogues
PS	Claim 4: Page 35-37; 45pp; English.
CC	This sequence represents a novel oestrogen binding protein isolated from
CC	human testis cDNA in order to study upstream translation-initiation
CC	codons using 5' RACE-PCR technology. This receptor is able to bind and
CC	be activated by estradiol, estrone and estrinol, can be used in a screening
CC	assay for the identification of new drugs e.g. novel ligands or hormonal
CC	analogues.
SQ	Sequence 530 AA:
Query Match	100.0%; Score 3904; DB 28; Length 530;
Best Local Similarity	100.0%; Pred. No. 0.00e+00;
Matches 530; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Dh	1 mdiknspslinspsysncsqsliplehgslylpsyydsihyepantfyepavmnyisps 60
Qy	1 MDIKNSPSSLNPSSTSYNCQSIIPLEHGSITIPSSYDSHHEPAMFYPAVNVNYSIPS 60
Dh	61 nvnchleqpgprgttsprvlpwptgshsplyvvhqqlshlyepqkspvcearslehtlpvn 120
Qy	61 NVNLEEGPGRQRTSPRVLPWPTGHSPLVYVHQLSHLYAEPOKSPCEARSLEHTLPVN 120
Dh	121 retlkrvsgnrcaspytgskxrdrdhfcaevcsdyagvyhygvwscgcgcaffkrsgqh 180
Qy	121 retlkrvsgnrcaspytgskxrdrdhfcaevcsdyagvyhygvwscgcgcaffkrsgqh 180

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QY 121 RETLKKRVSGNRKASPVTPGSGKRDAHFCACVSDYASGTYHGWSCBCKAFKRSIOGH 180
Db 181 ndylcpalnqctldknrrksqacrlrkcyegvmkcgrrercgylvrrgrsadeqlh 240
QY 181 NDYICPATNQCITIDKRRKSCQACRLRKCYEGVMKCGSRRERCGYLRVRRORSADQLH 240
Db 241 cagfakrsggghaprvrellldalspeqlvltllepphvlisrpsaefteasmmsltk 300
QY 241 CAGAKRSGGHAHPRVRELLDLALSPQLVLTLLPEPHVLISRPSAFTEASMMSLTk 300
Db 301 ladekylmismwakkipgfvelsfldqvrllscwmevllmgllmrsldhpkllfapdl 360
QY 301 LADKELVIMISMAKKIPGFVELSFLDQVRLLSCWMEVLLMGMLMRSIDHPEKLIFFADL 360
Db 361 vldfdegkcvgeglleifdmllattsrfrelklqhkelylcvkamllnssmyplvtatqda 420
QY 361 VLDRDEGKCVGEGLIEIFDMLATTSRFRELKQHKELYLCVKAMILLNSMYPVLTATQDA 420
Db 421 dsstklahllnavtdalvwiaksgisgqgmllanllmshvrhaskgmehllmkk 480
QY 421 DSSRLAHLNAVTDALVWIAKSGISSQOQSMRLANLMLSHVRHASKGMEHLNMK 480
Db 481 cknvpyvdllemnahvlgckssitgscspaedsksgsqnpsq 530
QY 481 CKNVPYVDLLEMLNAHVLRCKSSITGSECSPAEDSKSGSQNPSQ 530

RESULT 2
ID W14724 standard; Protein; 485 AA.
AC W14724:
DE 08-JUN-1997 (first entry)
DT Human oestrogen receptor beta (ER-beta).
KW Orphan receptor; oestrogen receptor beta; ER-beta;
  nuclear receptor; prostate cancer; benign prostatic hyperplasia;
  ovary cancer; cardiovascular disease; osteoporosis;
  environment; pollutant.
OS Homo sapiens.
FT Key Location/Qualifiers
FT domain 104..169
FT domain /label=DNA-binding_domain
FT domain 260..457
FT domain /label=Ligand-binding_domain
FN W09709348-A2.
PD 13-MAR-1997.
PR 09-SEP-1996; E03933.
PR 08-SEP-1995; GB-018272.
PR 15-MAR-1996; GB-005550.
PR 11-APR-1996; GB-007532.
PR 08-MAY-1996; GB-009576.
PA (KARO-) KARO BIO AB.
PI Emma E, Gustafsson J, Kulper GG;
DR N-PSDB: T62843.
DR WPI: 97-192842/17.
DE New isolated oestrogen receptor beta - used to develop prods. for
  treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
  disease
FT Claim 1; Fig 13A; 45bp; English.
PS A novel human orphan receptor (W14724) is related to the known
  oestrogen receptor ER-alpha, and has been designated ER-beta.
CC It is an oestrogen receptor-related nuclear receptor. The ER-beta
  amino acid sequence was deduced from a cDNA clone (T62843) isolated
  from a human testis cDNA library. Rat, human and mouse ER-beta
  (W14723-25) can be used to isolate molecules for use in the
  treatment of cardiovascular diseases, central nervous system
  diseases, osteoporosis, prostate or ovarian cancer or benign
  prostatic hyperplasia and to test environmental chemicals for
  oestrogenic activity.
CC Sequence 485 AA;

```

Query Match 91.8%; Score 3582; DB 21; Length 485;
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 mtfyspavmmslpsnvtlnlegpgqrqttspnvlwptpgphlspilvhrqlshlyaeqps 60
QY 46 MTFYSPAVMMSLPSNVTNLEGPGQRQTTSPTNVLWPTPGPHLSPIVHRQLSHLYAEQPS 105
Db 61 pwcarslehtlpvnretlkrkvsgnrcasvtpbgskrdahfcavcasyhygws 120
QY 61 PWCARSLEHTLPVNRRLKRVKSGNRCASVTPBGSKRDHFPACVCSDYASGTYHGWWS 165
Db 106 pwcarslehtlpvnretlkrkvsgnrcasvtpbgskrdahfcavcasyhygws 165
QY 106 PWCARSLEHTLPVNRRLKRVKSGNRCASVTPBGSKRDHFPACVCSDYASGTYHGWWS 165
Db 121 ceegkafkrszlgghndylcpalnqctldknrrksqacrlrkcyegvmkcgrrercg 180
QY 121 CEGKAFKRSZLGGHNDYICPATNQCITIDKRRKSCQACRLRKCYEGVMKCGSRRERCG 225
Db 166 CEGKAFKRSZLGGHNDYICPATNQCITIDKRRKSCQACRLRKCYEGVMKCGSRRERCG 225
QY 166 CEGKAFKRSZLGGHNDYICPATNQCITIDKRRKSCQACRLRKCYEGVMKCGSRRERCG 225
Db 181 yrlvrrgrsadeqlhcgagkrrsgghaprvrellldalspeqlvltllepphvlisr 240
QY 181 YLRVRRORSADQLHCGAKRSGGHAHPRVRELLDLALSPQLVLTLLPEPHVLISRP 285
Db 226 yrlvrrgrsadeqlhcgagkrrsgghaprvrellldalspeqlvltllepphvlisr 285
QY 226 YLRVRRORSADQLHCGAKRSGGHAHPRVRELLDLALSPQLVLTLLPEPHVLISRP 285
Db 241 sapfteasmmslrlkladkelvhwakkipgfvelsfldqvrllscwmevllmgllm 300
QY 241 SAPFTEASMMSLRLKLADKELVHWAKKIPGFVELSFLDQVRLLSCWMEVLLMGMLM 345
Db 286 SAPFTEASMMSLRLKLADKELVHWAKKIPGFVELSFLDQVRLLSCWMEVLLMGMLM 345
QY 286 SAPFTEASMMSLRLKLADKELVHWAKKIPGFVELSFLDQVRLLSCWMEVLLMGMLM 345
Db 301 rsldhpgkllfapdlvldfdegkcvgeglleifdmllattsrfrelklqhkelylcvkam 360
QY 301 RSIDHPGKLIFAPDLVLDREKCVGEGLIEIFDMLATTSRFRELKQHKELYLCVKAMIL 405
Db 346 RSIDHPGKLIFAPDLVLDREKCVGEGLIEIFDMLATTSRFRELKQHKELYLCVKAMIL 405
QY 346 RSIDHPGKLIFAPDLVLDREKCVGEGLIEIFDMLATTSRFRELKQHKELYLCVKAMIL 405
Db 361 lnssmyplvtatqdasstklahllnavtdalvwiaksgisgqgmllanllmshvrhask 420
QY 361 LNSSMYPVLTATQDASSRLAHLNAVTDALVWIAKSGISSQOQSMRLANLMLSHV 465
Db 421 rhasnkgmehllmkkcknvpyvdllemnahvlgckssitgscspaedsksgsq 480
QY 421 RHASKGMEHLNMKCKNVPYVDLLEMLNAHVLRCKSSITGSECSPAEDSKSGSQ 525
Db 481 nlqsg 485
QY 481 NLQSG 530

```

```

RESULT 3
ID W33212 standard; Protein; 477 AA.
AC W33212:
DE 20-APR-1998 (first entry)
DT Human oestrogen receptor protein.
DE Oestrogen receptor protein; steroid; alternative splicing; estradiol;
  KW estrogen; estrinol; screening.
OS Homo sapiens.
FT Key Location/Qualifiers
FT domain 1-798378-A2.
PD 01-OCT-1997.
PR 25-MAR-1997; 200903.
PR 22-NOV-1996; EP-203284.
PR 26-MAR-1996; EP-200820.
PA (ALKU) AKZO NOBEL NV.
PI Dijkema R, Mosseelman S;
DR WPI: 97-473188/44.
DE DNA encoding estrogen receptor - useful in screening assay to
  identify novel ligands or hormonal analogues
FT Identically novel ligands or hormonal analogues
PS Claim 4; Page 18-20; 45bp; English.
CC This sequence represents a novel oestrogen binding protein. The cDNA
  sequence which encodes this protein can be alternatively spliced
  resulting in the detection of additional transcripts (see T88413).
CC This receptor is able to bind and be activated by estradiol, estrogen
  and estrinol, can be used in a screening assay for the identification of new
  drugs e.g. novel ligands or hormonal analogues.
CC Sequence 477 AA;

```

Query Match 90.5%; Score 3532; DB 28; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 ehlpvnrcltkrvsgnrcaspytpgskrdahfcavcdsyasyhyvscgcakaff 120
 QY 114 EHLTPVNRCLTKRVSGNRCASPYTPGSKRDHFCVCSDYASGYHYVSCGCAKAF 173
 Db 121 krsigghndyicpatngctldknrrkscgacrlrkcyevmvgcgsrrercgyrlvrrgr 180
 QY 174 KRSIGGHNDYICPATNGCTLDKNRRKSCGACRLRKCYEVMVGCSRRERCGRVLRGR 223
 Db 181 sadeqlhcasgkaksrghaprvrellldalspeqlvlllaepphyllsrpafteas 240
 QY 234 SADEQLHCAGKAKSRGSHAPRVRELLLDALSPQQLVTLLEAPPHVLSRPAFTFEAS 223
 Db 241 mmmstlkladkelvnmisvaakkipgfvelslfdqvrllscwmevllmnglmwrsidhpgk 300
 QY 294 MMSSTLKLADKELVNMISVAAKKIPGFVELSLFDQVRLLESCWMEVLLMNGLMWRSIDHPGK 353
 Db 301 ltfapdlvdrdegkveglleifdmllatstfrfrelklqhkelylcvkamlllnsmnrypl 360
 QY 354 LTFAPDLVDRDEGKVEGLEIFDMLLATSTFRRELKLQHKELYLCVKAMILLNNSMYPL 413
 Db 361 vlatqdadssrklahlinavtalvwwiaksgisgsgqsmtlanllmllshvrhasnkgm 420
 QY 414 VLATQDADSSRKLAHLINAVTDALVWVIAKSGISSQOQSMRLANLMLLSHVHASNKG 473
 Db 421 ehllmckknvpyd11lemlnahvltgckssltgsecspsadsksksgsqnpgsq 477
 QY 474 EHLNMCKKNVYPYD11LEMLNAHVLTGCKSSLTGSECSPADSKSKSGSQNPQSQ 530

RESULT 4
 W14723 standard; Protein: 485 AA.

AC W14723;
 DE 08-JUN-1997 (first entry)
 DE Rat oestrogen receptor beta (ER-beta).
 KW Orphan receptor; oestrogen receptor beta; ER-beta;
 KW nuclear receptor; prostate cancer; benign prostatic hyperplasia;
 KW ovary cancer; cardiovascular disease; osteoporosis;
 KW environment; pollutant.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT domain 104..169
 FT /label= DNA-binding_domain
 FT domain 259..457
 FT /label= Ligand-binding_domain
 PN WO9709348-A2.
 PD 13-MAR-1997.
 PR 09-SEP-1996; E03933.
 PR 08-SEP-1995; GB-018272.
 PR 15-MAR-1996; GB-005550.
 PR 11-APR-1996; GB-007532.
 PR 08-MAY-1996; GB-009576.
 PA (KARO-) KARO BIO AB.
 PI Enmark E, Gustafsson J, Kuiper GG;
 DR WPI: 97-192842/17.
 DR N-PSDB: T62844.
 PT New isolated oestrogen receptor beta - used to develop prods. for
 PT treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
 PT disease
 PS Claim 1; Fig 1; 45pp; English.
 CC A novel rat orphan receptor (W14723) is related to the known
 CC oestrogen receptor ER-alpha, and has been designated ER-beta.
 CC It is an oestrogen receptor-related nuclear receptor. The ER-beta
 CC amino acid sequence was deduced from a cDNA clone (T62842) isolated
 CC from a rat prostate cDNA library. Rat, human and mouse ER-beta
 CC (W14723-25) can be used to isolate molecules for use in the
 CC treatment of cardiovascular diseases, central nervous system
 CC diseases, osteoporosis, prostate or ovarian cancer or benign
 CC prostatic hyperplasia and to test environmental chemicals for
 CC oestrogenic activity.
 CC Sequence 485 AA.

Query Match 83.9%; Score 3274; DB 21; Length 485;
 Best Local Similarity 88.7%; Pred. No. 0.00e+00;

Matches 430; Conservative 35; Mismatches 20; Indels 0; Gaps 0;
 Db 1 mtfysaammyvsgstsladggpvlrlstspnlytpstgshlpalabqsslllyapqks 60
 QY 46 MTFYSAAMMYVSGSTSLADGGPVLRLSTSPNLYTPSTGSHLPALABQSSLLYAPQKS 105
 Db 61 pwcarslehtlpvnrcltkrksigscaspytspnkrdahfcpvcsdyasyhyvgs 120
 QY 106 PWCARSLEHTLPVNRCLTKRKSIGSCASPYTSPNKRDAHFCVCSDYASGYHYVGS 165
 Db 121 cegeckaftrsigghndyicpatngctldknrrkscgacrlrkcyevmvgcgsrrercg 180
 QY 166 CECECKAFTRSIGGHNDYICPATNGCTLDKNRRKSCGACRLRKCYEVMVGCSRRERC 225
 Db 181 yrlvrrorsadepohcagakrakgshaprvrellldalspeqlvlllaepphyllsrp 240
 QY 226 YRLVRRORSADepohCAGAKRKGSHAPRVRELLLDALSPQQLVTLLEAPPHVLSR 285
 Db 241 smpfteasmmmsltkladkelvnmisvaakkipgfvelslfdqvrllscwmevllmnglmw 300
 QY 286 SAMPFTEASMMMSLTKLADKELVNMISVAAKKIPGFVELSLFDQVRLLESCWMEVLLMNG 345
 Db 301 rsidhpgkllfapdlvdrdegkveglleifdmllatstfrfrelklqhkelylcvkamll 360
 QY 346 RSIDHPGKLLFAPDLVDRDEGKVEGLEIFDMLLATSTFRRELKLQHKELYLCVKAM 405
 Db 361 lnsmnryplvlatqdadssrklahlinavtalvwwiaksgisgsgqsmtlanllmllshv 420
 QY 406 LNSMRYPLVLATQDADSSRKLAHLINAVTDALVWVIAKSGISSQOQSMRLANLMLLSHV 465
 Db 421 rthsnkghemllsmckknvpyd11lemlnahvltgckssltgsecspsadsksksgsqnpgsq 480
 QY 466 RTHSNKGHEMLLMCKKNVYPYD11LEMLNAHVLTGCKSSLTGSECSPADSKSKSGSQ 525
 Db 481 nlqsg 485
 QY 526 NPQSQ 530

RESULT 5
 W14725 standard; Protein: 485 AA.

AC W14725;
 DE 08-JUN-1997 (first entry)
 DE Mouse oestrogen receptor beta (ER-beta).
 KW Orphan receptor; oestrogen receptor beta; ER-beta;
 KW nuclear receptor; prostate cancer; benign prostatic hyperplasia;
 KW ovary cancer; cardiovascular disease; osteoporosis;
 KW environment; pollutant.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT domain 104..169
 FT /label= DNA-binding_domain
 FT domain 260..457
 FT /label= Ligand-binding_domain
 PN WO9709348-A2.
 PD 13-MAR-1997.
 PR 09-SEP-1996; E03933.
 PR 08-SEP-1995; GB-018272.
 PR 15-MAR-1996; GB-005550.
 PR 11-APR-1996; GB-007532.
 PR 08-MAY-1996; GB-009576.
 PA (KARO-) KARO BIO AB.
 PI Enmark E, Gustafsson J, Kuiper GG;
 DR WPI: 97-192842/17.
 DR N-PSDB: T62844.
 PT New isolated oestrogen receptor beta - used to develop prods. for
 PT treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
 PT disease
 PS Claim 1; Fig 14A; 45pp; English.
 CC A novel mouse orphan receptor (W14725) is related to the known
 CC oestrogen receptor ER-alpha, and has been designated ER-beta.
 CC It is an oestrogen receptor-related nuclear receptor. The ER-beta
 CC amino acid sequence was deduced from a cDNA clone (T62844).

CC Rat, human and mouse ER-beta (M14723-25) can be used to isolate
CC molecules for use in the treatment of cardiovascular diseases,
CC central nervous system diseases, osteoporosis, prostate or ovarian
CC cancer or benign prostatic hyperplasia and to test environmental
CC chemicals for oestrogenic activity.
SQ Sequence 485 AA;

Query Match 83.2%; Score 3250; DB 21; Length 485;

Best Local Similarity 88.0%; Pred. No. 0.00e+00;

Matches 427; Conservative 36; Mismatches 22; Indels 0; Gaps 0;

```
Db 1 mafyspawmyvpsstgnllegpvrqtaapnvlwpsghlslatcgssllyaepqks 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 46 MTFESPVMNYSIPSNVTNLEGGGPGRTSPNLMPTFGHLSPLVHROLSHLYAEPOKS 105
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 pmcearslehlprnreltkrkllgsgcasptspstckrdahfcavcsgdyasgyhyvws 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 106 pmcearslehlprnreltkrkllgsgcasptspstckrdahfcavcsgdyasgyhyvws 165
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 cecgkafkrsigghndyicpatnqctldknrtkscgacrlrkcyevgmvcgsrrercg 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 166 CEGKAFKRSIGGHNDYICPATNCTIDKNRRKSCQCRLRKCYEVMVCGSRRERCG 225
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 yrlvrrgrsasegyhclnkakrtsgnprvke|||nslspeqlv|||laeppnvlstrp 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 226 YRLVRGRSADQLHCAGKAKRSQGHAPRVRELLDALSPQLVTLLEAPPHVLSRP 285
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 smptfssmmmslkladkelvhlmgvakk:ipgfvelslfdqvrllscemvevmgmw 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 286 SAPTESSMMMSLTKLADKELVHMTSMWAKKIPGFVELSLFDQVRLLSCMVEVLMGMW 345
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 rsihpgkllfapdlvldrdegkcevglllelfdmlattarfelkqhkeylcvkamll 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 346 RSIDHPGKLIRAPDLVDRDEGKCEVGLLEIFDMLATTSSRFELKQHKKEYLCKAMIL 405
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 lnsmyhlatasgeesrklthlnavtdalvwvksrissgsgqsmrlnllmshv 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 406 LNSMYRPLVYATODASSRKLHLNVAVTDALVWVIAKSGISSQOOSMRNLMLLSHV 465
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 rhiisnkgnehlismckkvpyvdlllmlahltlrgkssissgsgcstsskegsq 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 466 RHASNKGEHLNMCCKNVVYDILLMLNHNHVRGCKSSITGSECPAEDSKSKESSQ 525
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 481 nlgsq 485
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 526 NPQSQ 530
```

RESULT 6
ID W33213 standard; Protein; 416 AA.

AC W33213;
DT 20-APR-1998 (first entry)
DE Human oestrogen receptor protein exon 8 splice variant.
KW Oestrogen receptor protein; steroid; alternative splicing; estradiol;
KW estrone; estrinol; screening.
OS Homo sapiens.
PN EP-798378-A2.
PI 01-OCR-1997.
PD 25-MAR-1997; 200903.
PR 22-NOV-1996; EP-203284.
PR 26-MAR-1996; EP-200820.
PA (ALKU) AKZO NOBEL NV.
PI DiJkema R, Mosselman S;
DR WPI: 97-473188/44.
N-PSDB: T88413.
PT DNA encoding estrogen receptor - useful in screening assay to
PT identify novel ligands or hormonal analogues
PS Claim 4; Page 20-22; 45pp; English.
CC This partial sequence represents a splice variant of a novel oestrogen
CC binding protein, detected by screening a human testis cDNA library.
CC This protein contains an alternative exon 8 (exon 8B) of the novel
CC oestrogen receptor represented. As a consequence of the introduction of
CC this exon through an alternative splicing reaction, the reading frame

CC encoding the novel receptor is immediately terminated, creating a
CC truncation of the carboxy terminus of the novel receptor. This receptor
CC is able to bind and be activated by estradiol, estrone and estrinol, can be
CC used in a screening assay for the identification of new drugs e.g. novel
CC ligands or hormonal analogues. This variant does not contain an Af-2
CC region and therefore probably lacks the ability to modulate transcription
CC of target genes in a ligand dependent fashion.
SQ Sequence 416 AA;

Query Match 79.4%; Score 3099; DB 27; Length 416;

Best Local Similarity 100.0%; Pred. No. 4.32e-293;

Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db 1 mnyisnvnlnlegpqrqtsppnvlwptpghlslvlnhqlshlyaeqkspwcearsl 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 54 MNYSIPSNVTNLEGGGPGRTSPNLMPTFGHLSPLVHROLSHLYAEPOKSPWCEARSL 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ehllprnreltkrkvgncrcaapvtgpgskrdahfcavcsgdyasgyhyvwscegkaff 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 114 EHLLPVNRETLKRRKVSQNRCAAPVTGPGSKRDHAFCAVCSGYHYGVWSCEGKAF 173
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 krsigghndyicpatnqctldknrtkscgacrlrkcyevgmvcgsrrercgyrlvrrgr 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 174 KRSIGGHNDYICPATNCTIDKNRRKSCQCRLRKCYEVMVCGSRRERCGYRLVRGR 233
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 sadeqlhcaqkkrsgghaprvrellldalspeqlv|||laeppnvlstrpafteas 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 234 SADQLHCAGKAKRSQGHAPRVRELLDALSPQLVTLLEAPPHVLSRPAPTEAS 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 mmslrlkladkelvhlmgvakk:ipgfvelslfdqvrllscemvevmgmwlmvrsidhpgk 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 294 MMSLRLKLADKELVHMTSMWAKKIPGFVELSLFDQVRLLSCMVEVLMGMMSIDHPGK 353
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 llfapdlvldrdegkcevglllelfdmlattsrfrfelkqhkeylcvkamllnssmypl 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 354 LIRAPDLVDRDEGKCEVGLLEIFDMLATTSSRFELKQHKKEYLCKAMILNSSMYPL 413
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 vtatqdasrklahlhlnavtdalvwvksrissgsgqsmrlnllmshvzha 415
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 414 VTATQDASSRKLHLNVAVTDALVWVIAKSGISSQOOSMRNLMLLSHVZHA 468
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 7
ID W33214 standard; Protein; 418 AA.

AC W33214;
DT 20-APR-1998 (first entry)
DE Human oestrogen receptor protein splice variant (exon 8C).
KW Oestrogen receptor protein; steroid; alternative splicing; estradiol;
KW estrone; estrinol; screening.
OS Homo sapiens.
PN EP-798378-A2.
PI 01-OCR-1997.
PD 25-MAR-1997; 200903.
PR 22-NOV-1996; EP-203284.
PR 26-MAR-1996; EP-200820.
PA (ALKU) AKZO NOBEL NV.
PI DiJkema R, Mosselman S;
DR WPI: 97-473188/44.
N-PSDB: T88414.
PT DNA encoding estrogen receptor - useful in screening assay to
PT identify novel ligands or hormonal analogues
PS Claim 4; Page 30-32; 45pp; English.
CC This sequence represents a splice variant of a novel oestrogen binding
CC protein isolated from human thymus tissue. This protein contains an
CC alternative exon 8 (exon 8C) of the novel oestrogen receptor represented
CC in T88412. This novel receptor is able to bind and be activated by
CC estradiol, estrone and estrinol, can be used in a screening assay for the
CC identification of new drugs e.g. novel ligands or hormonal analogues.
CC This variant does not contain an Af-2 region and therefore probably
CC lacks the ability to modulate transcription of target genes in a ligand
CC dependent fashion.
SQ Sequence 418 AA;

Query Match 79.4%; Score 3099; DB 28; Length 418;
 Best Local Similarity 100.0%; Pred. No. 4,32e-293;
 Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mnyispsnvnleegpqrptspnvlwptphlpvlvhrhgllvyeepkspcearsl 60
 |||||
 Qy 54 MNYISPSNVNLEEGPGRPTTSPVNLWPTPHLSPLVYHRLSHLVEPKSPMCEARSL 113
 |||||

Db 61 ehtlpvnetlkrkvsngarcsapvtgprskrdahfcavcsdyagynhyvscgckaff 120
 |||||
 Qy 114 EHTLPVNETLKRKVSNGARCSAPVTGPRSKRDHFCVAVCSDYAGYHYVSCGCKAFF 173
 |||||

Db 121 krsiqgmndyicpatnctldknrrkscgacrlkcyevgmwkcgsrrecgylrvtrqr 180
 |||||
 Qy 174 KRSIQGMNDYICPATNCTIDKNRRKSCOACRLKCYEVGMWKCGRRECGYRLVRQR 233
 |||||

Db 181 sadedqlhacgkkrsggghaprvrelldalspeqlvltlleaephylisrpsapfcea 240
 |||||
 Qy 234 SADEDQLHACGKAKRSGGHAPRVRELLDALSPEDLVLTLEAEPHYLISRPSAPFEAS 293
 |||||

Db 241 mmsstklackelyhmiswakkipgfvelsifdgvrllscemewlmvglmwrsidhpgk 300
 |||||
 Qy 294 MMSSTKLADKELVHMTSMAKKIRGFVELSIFDQVRLLESCMEVLMGLMKMRSIDHPRK 353
 |||||

Db 301 ltfapdlvldrddegkveglleifdmllatsrfrelkqhkeylcvkamllnssmypi 360
 |||||
 Qy 354 LTFAPDLVLDREDEKVEGLEIFDMLLATSRFRELKQKEYLCVKAMILLNSSMYP 413
 |||||

Db 361 vtttqddssrklahlnavtdaivwriaksglssggqgmrlanllmshvrha 415
 |||||
 Qy 414 VTATQDDSSRKLALHNLNAVTDALVWRIAKSGISSGQGMRLANLLMLSHVRA 468
 |||||

RESULT 8
 ID W33211 standard; protein; 233 AA.
 AC W33211;
 DT 20-APR-1998 (first entry)
 DE Human oestrogen receptor protein ligand binding domain.
 KW Oestrogen receptor protein; steroid; estradiol; estrone; estrinol;
 OS screening; ligand binding domain.
 PS Homo sapiens.
 PN EP-798378-A2.
 PD 01-OCT-1997.
 PE 25-MAR-1997; 200903.
 PR 22-NOV-1996; EP-203284.
 RA 26-MAR-1996; EP-200820.
 PA (ALU) AKZO NOBEL NV.
 PI Dijkema R, Mosselman S;
 DR N-PDB: T88412.
 PT DNA encoding estrogen receptor - useful in screening assay to
 PS identify novel ligands or hormonal analogues
 PS Claim 4; Page 16-17; 45pp; English.
 CC This sequence encodes the ligand binding domain of a novel
 CC oestrogen binding protein, detected by screening a human testis
 CC cDNA library. This receptor is able to bind and be activated by
 CC estradiol, estrone and estrinol, can be used in a screening assay for
 CC the identification of new drugs e.g. novel ligands or hormonal
 CC analogues.
 CC Sequence 233 AA;

Query Match 43.9%; Score 1714; DB 27; Length 233;
 Best Local Similarity 99.6%; Pred. No. 2,24e-154;
 Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 lvltlleaephylisrpsapfceaasmmslklackelyhmiswakkipgfvelsifdg 60
 |||||
 Qy 268 LVLTLEAEPHYLISRPSAPFEASMMSTLKLADKELVHMTSMAKKIRGFVELSIFDQ 327
 |||||

Db 61 vrlleescmewlmvglmwrsidhpgkllfapdlvldrddegkveglleifdmllatsrf 120
 |||||
 Qy 328 VRLLESCMEVLMGLMKMRSIDHPRKLTIFAPDLVLDREDEKVEGLEIFDMLLATSRF 387
 |||||

Db 121 relkqhkeylcvkamllnssmypiylatcgdaassrklahlnavtdaivwriaksgis 180
 |||||
 Qy 388 RELKQKEYLCVKAMILLNSSMYPYLATQDDSSRKLALHNLNAVTDALVWRIAKSGIS 447
 |||||

Db 181 sqggsmrlanllmshvrhaakgmehllnmcknvpywdlllemnahvl 233
 |||||
 Qy 448 SQOOSMRLANLLMLSHVRAHNSKGMHELLNMCKNVVYDLELLEMLNAHVL 500
 |||||

RESULT 9
 ID P70543 standard; protein; 595 AA.
 AC P70543;
 DT 24-FEB-1991 (first entry)
 DE Human oestrogen receptor protein.
 KW Human oestrogen receptor protein; expression system; assay.
 OS Homo sapiens.
 PN W08705049-A.
 PD 27-AUG-1987.
 PE 18-FEB-1987; U00341.
 PR 20-FEB-1986; US-833829.
 PA (CALB-) California Biotechnology Inc.
 PI Shine J;
 DR WPI: 87-250213/35.
 DR N-PDB: N70880.
 PT Expression system for vertebrate steroid receptor protein - comprising
 PT DNA sequence encoding the protein linked to control sequences in
 PT eucaryotic hosts.
 PS Disclosure; Fig. 1-1 - 1-2; 26pp; English.
 CC Steroid receptor protein;
 CC The protein is expressed in an expression system from cDNA operably
 CC linked to control sequences compatible with eukaryotic host cells.
 CC This method allows expression under conditions which favour appropriate
 CC post-translational processing. It also produces large amts. of purified
 CC protein useful in the design of agonist and antagonist cpsds. for study
 CC of the mechanism of action of the steroid binding proteins in general,
 CC and for use in diagnostic assays for the proteins or antibodies to
 CC them. These assays are important in, eg the diagnosis of tumour
 CC sensitivities to steroid metabolism. Suitable host cells are VERO,
 CC HeLa and CHO cells.
 CC Sequence 595 AA;

Query Match 42.8%; Score 1671; DB 2; Length 595;
 Best Local Similarity 56.3%; Pred. No. 4,30e-150;
 Matches 227; Conservative 98; Mismatches 61; Indels 17; Gaps 13;

Db 178 saketycavcndyagsgyhygvscgckafkrsiqgmndymcpatnctldknrrksc 237
 |||||
 Qy 142 SKRDAHRCVAVCSDYAGYHYGVSCGCKAFKRSIQGMNDYICPATNCTIDKNRRKSC 201
 |||||

Db 238 gaerlkcyevgmwkmqgikldrrgtrmlkhrqrddeggrgvegsagdmraanlwpsslm 297
 |||||
 Qy 202 QACRLKRCYEVGMWKCGRRECGYRLVR--RORSAD-QLHOCAGRA-KRSGG--HAP-R 254
 |||||

Db 298 lkrskksnslstltdagmvsalldaapp-llseybptprfseasmglltnladrelvh 356
 |||||
 Qy 255 V-KEL--LD-ALSPEDLVLTLEAEPHYLISR--PSAPFEASMMSTLKLADKELVH 308
 |||||

Db 357 mlnwkrvpgfvdlclhdqghlllecawlellmiglvrwsmehpvkllfapanllidrnqgk 416
 |||||
 Qy 309 MISMAKKIRGFVELSIFDQVRLLESCMEVLMGLMKMRSIDHPRKLTIFAPDLVLDREDEK 368
 |||||

Db 417 cvegmveifdmllatsrfrmmnlgeeefvclsklllnsgvytlfslstksleekdh 476
 |||||
 Qy 369 CVEGIEIFDMLLATSRFRELKQKEYLCVKAMILLNSSMYPYLATQDA--DSSRKL 427
 |||||

Db 477 rvidkltidtlhmakarlltggqghrqlajlllshtrmsnkgmehlymcknvpy 536
 |||||
 Qy 428 HLNAVTDALVWRIAKSGISSOQSMRLANLLMLSHVRAHNSKGMHELLNMCKNVVY 487
 |||||

Db 537 ydlillemlahrlha-ptsrgasveedqshlatatsashs 578
 |||||
 Qy 488 YDILLEMLNAHVLRGCKSSITGSECPADDSK-SKSGSQNPQS 529
 |||||

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RESULT 10
ID P80925 standard; protein; 334 AA.
AC P80925:
DE 29-DEC-1990 (first entry)
DE Sequence of the human oestrogen receptor
KW Hormone receptor; hormone-binding.
OS Homo sapiens.
PN WO8803168-A.
PD 05-MAY-1988.
PE 23-OCT-1987; US-108471.
PR (Salk) Salk Inst for Biol Stud.
PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V;
DR WPI; 88-133242/19.
DR N-PSDB; N80922.
PT Recombinant DNA encoding hormone receptors -
PT comprising glucocorticoid, mineralocorticoid, thyroid hormone
PT and novel hormone receptors
PS Example; Fig III-2; 243pp; English.
CC DNAs encoding hormone receptors and the hormone receptors themselves are
CC claimed. The DNA can be used to make the hormone receptor proteins and
CC functional modified forms in quantities not previously possible. The
CC receptor proteins can be used to screen cpts. for receptor-agonist or
CC receptor-antagonist activity. They can also be used in diagnostic assays.
SQ Sequence 334 AA;

Query Match 36.5%; Score 1424; DB 2; Length 334;
Best Local Similarity 57.4%; Pred. No. 1,58e-125;
Matches 193; Conservative 80; Mismatches 47; Indels 16; Gaps 12;

Db 1 ycaavcdasygyhyvvascegcakfkts-qghndymcpatnctidknrtkscgacrlr 59
QY 148 FCACVSDYASGYHYGVWSCGCGCAFFKRSIOGHNDYICPATNCTIDKNRRSCQACRLR 207
Db 60 kcytgmkmkggikrtggrlmkhhkrqddgggrgvgvsagdmzamlwpspdlmkkzsk 119
QY 208 KCYEGVMKCGSRRECGRLVR--RQNSADG-QLHCAGKA-KRSGG--HAF-RV-RELL 259
Db 120 nslalsladgmvsalldaerp-ilyeydprtrfseasmglalnadrelvhlmwak 178
QY 260 --LD-ALSPEDVLTLLEAFPHVLSR--PSAPTEASMMSLTKLADKELVHISMNAK 314
Db 179 tvpgrfdltlndqvhlllecaulelmiglwtrsmehpvyklfapnllldrngkcvemv 238
QY 315 KIPGEVELSLFDQVRLSLSCWMEVLMGMLMRSIDHPGKLIPADLVLDROGKCEGTL 374
Db 239 eifdmllstsrfrmmnlqgeefvclkslllinsgyvflstlksleekdhvhvldki 298
QY 375 EIEFDMLLSTSRFRRLKIQHKEYLQVKAMILLNSSMYPLVATODA-DSSRKLHLNNAV 433
Db 299 tdtllhmakagltlqqghqrlaqllllshirhms 334
QY 434 TDAIYVWYIAKSGSISSQOQSMRLANLMLLSHRHMS 469

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PS Claim 17; Fig V-2(B)-1 and -2; 243pp; English.
CC DNAs encoding hormone receptors and the hormone receptors themselves are
CC claimed. The DNA can be used to make the hormone receptor proteins and
CC functional modified forms in quantities not previously possible. The
CC receptor proteins can be used to screen cpts. for receptor-agonist or
CC receptor-antagonist activity. They can also be used in diagnostic assays.
CC Also claimed is pure DNA encoding oestrogen-related receptors hERR1 and
CC hERR2 and hERR1 and hERR2. The new hERR1 and hERR2 receptors will provide
CC the basis for development of an assay system that will lead to the
CC identification of novel hormones.
SQ Sequence 433 AA;

Query Match 20.7%; Score 807; DB 2; Length 433;
Best Local Similarity 39.5%; Pred. No. 1,04e-64;
Matches 140; Conservative 84; Mismatches 108; Indels 22; Gaps 14;

Db 101 rlcvcddasgyhyvvascegcakfkrtlignlieyscpatneceltkrtkscgacrf 160
QY 147 HFCACVSDYASGYHYGVWSCGCGCAFFKRSIOGHNDYICPATNCTIDKNRRSCQACRL 206
Db 161 mcklvgmlkegvldtr--f-ggrqky-krrldsenspylsqispakpklklys-- 214
QY 207 RKCYEGVMKCGSRRECGRLVRGRSADQLHCAGKARSGGHAPRVRELLDALSP 266
Db 215 yl-l-vaepdklyam--ppddvpegdlaltlcladrelvfliswakhlpgfnltd 271
QY 267 QLVTLLEAFPHVLSRPSAPTEASMMSLTKLADKELVHISMNAKPIGFEVELSLFD 326
Db 272 gmslllgsamealllglivysrlypyddklayaedymdeemslr-gllelyralqlvtr 330
QY 327 QVRLESQWMEVLMGMLMRSIDHPGKLIPADLVLDROGKCEGTLFDMLATTSR 386
Db 331 ykklkvekeefwmlkalalansdmy--l--enleavqkldllh--calq-dyels 380
QY 387 FRELKHKEYLCVKAMILLNS-SMYPLVATODAQSRLANLNVDTALVWYIAKSG 445
Db 381 -qrheeprragklllclprrlqtaakavqfysvklgqkpmhlflemleakv 433
QY 446 ISSQOQSMRLANLMLLSHRHMSNGMEHLNMKCRNVVYDLEMLNAV 499

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RESULT 12
ID P80930 standard; protein; 521 AA.
AC P80930:
DE 10-MAR-1993 (revised)
DE 29-DEC-1990 (first entry)
DE Sequence of human estrogen-related receptor protein (hERR1)
KW Hormone receptor; hormone-binding; transcription activation.
OS Homo sapiens.
PN WO8803168-A.
PD 05-MAY-1988.
PE 23-OCT-1987; US-108471.
PR (Salk) Salk Inst for Biol Stud.
PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V;
DR WPI; 88-133242/19.
DR N-PSDB; N80921.
PT Recombinant DNA encoding hormone receptors -
PT comprising glucocorticoid, mineralocorticoid, thyroid hormone
PT and novel hormone receptors
PS Claim 17; Fig V-1(B)-1 and -2; 243pp; English.
CC DNAs encoding hormone receptors and the hormone receptors themselves are
CC claimed. The DNA can be used to make the hormone receptor proteins and
CC functional modified forms in quantities not previously possible. The
CC receptor proteins can be used to screen cpts. for receptor-agonist or
CC receptor-antagonist activity. They can also be used in diagnostic assays.
CC Also claimed is pure DNA encoding oestrogen-related receptors hERR1 and
CC hERR2 and hERR1 and hERR2. The new hERR1 and hERR2 receptors will provide
CC the basis for development of an assay system that will lead to the
CC identification of novel hormones.
SQ Sequence 521 AA;

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Query Match 20.5%; Score 800; DB 2; Length 521;

